Full wwPDB EM Validation Report ⓘ

Apr 1, 2025 – 07:16 pm BST

PDB ID	:	5N5Y / pdb_00005n5y
EMDB ID	:	EMD-3590
Title	:	Cryo-EM structure of RNA polymerase I in complex with Rrn3 and Core Factor (Orientation III)
Authors	:	Engel, C.; Gubbey, T.; Neyer, S.; Sainsbury, S.; Oberthuer, C.; Baejen, C.; Bernecky, C.; Cramer, P.
Deposited on	:	2017-02-14
Resolution	:	7.70 Å(reported)

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references ⓘ) were used in the production of this report:

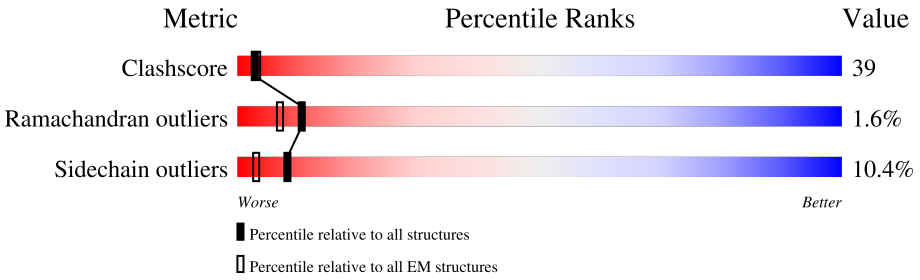
EMDB validation analysis	:	0.0.1.dev117
Mogul	:	1.8.4, CSD as541be (2020)
MolProbity	:	4.02b-467
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.42

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 7.70 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion < 40%). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	1664	9% 61% 24% 12%
2	B	1203	12% 64% 30%
3	C	335	5% 65% 23% 9%
4	D	137	31% 9% 58%
5	E	215	78% 17%
6	F	155	5% 48% 14% 35%
7	G	326	5% 43% 15% 41%
8	H	146	67% 21% 10%

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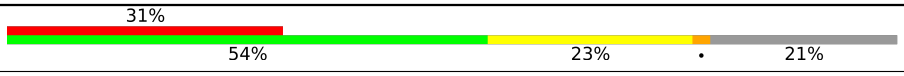
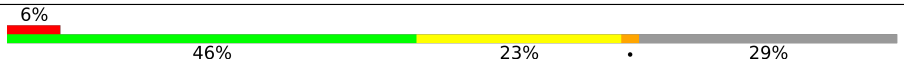
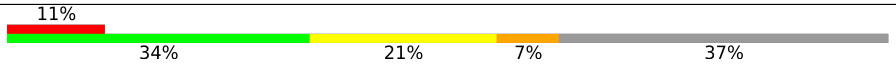
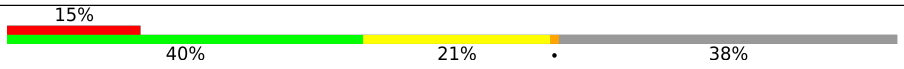
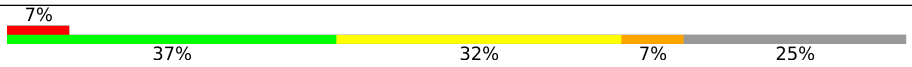
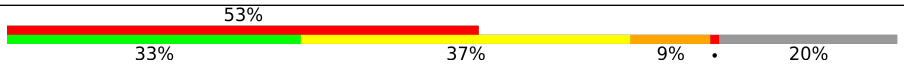
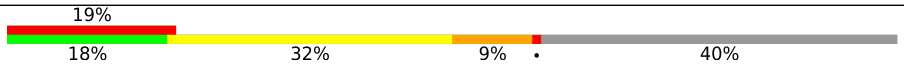
Mol	Chain	Length	Quality of chain
9	I	125	
10	J	70	
11	K	142	
12	L	70	
13	M	415	
14	N	233	
15	O	627	
16	P	894	
17	Q	514	
18	R	507	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
20	SO4	R	601	-	-	X	-

2 Entry composition

There are 21 unique types of molecules in this entry. The entry contains 48030 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called DNA-directed RNA polymerase I subunit RPA190.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	1467	11598	7327	2017	2193	61	0	0

- Molecule 2 is a protein called DNA-directed RNA polymerase I subunit RPA135.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	B	1172	9312	5891	1633	1738	50	0	0

- Molecule 3 is a protein called DNA-directed RNA polymerases I and III subunit RPAC1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	C	305	2423	1539	416	460	8	0	0

- Molecule 4 is a protein called DNA-directed RNA polymerase I subunit RPA14.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
4	D	58	459	289	78	92	0	0

- Molecule 5 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	E	212	1735	1102	306	316	11	0	0

- Molecule 6 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	F	100	823	522	144	154	3	0	0

- Molecule 7 is a protein called DNA-directed RNA polymerase I subunit RPA43.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	193	Total	C	N	O	S	0	0
			1526	985	262	274	5		

- Molecule 8 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC3.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	131	Total	C	N	O	S	0	0
			1052	664	176	208	4		

- Molecule 9 is a protein called DNA-directed RNA polymerase I subunit RPA12.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	99	Total	C	N	O	S	0	0
			755	472	125	149	9		

- Molecule 10 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC5.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	69	Total	C	N	O	S	0	0
			569	362	101	100	6		

- Molecule 11 is a protein called DNA-directed RNA polymerases I and III subunit RPAC2.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	101	Total	C	N	O	S	0	0
			793	496	130	162	5		

- Molecule 12 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC4.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	44	Total	C	N	O	S	0	0
			352	217	70	61	4		

- Molecule 13 is a protein called DNA-directed RNA polymerase I subunit RPA49.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	M	108	Total	C	N	O	0	0
			856	543	142	171		

- Molecule 14 is a protein called DNA-directed RNA polymerase I subunit RPA34.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	145	Total	C	N	O	S	0	0
			1151	735	188	224	4		

- Molecule 15 is a protein called RNA polymerase I-specific transcription initiation factor RRN3.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	473	Total	C	N	O	S	0	0
			3907	2533	642	711	21		

- Molecule 16 is a protein called RNA polymerase I-specific transcription initiation factor RRN6.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	P	583	Total	C	N	O	S	0	0
			4729	3010	803	905	11		

- Molecule 17 is a protein called RNA polymerase I-specific transcription initiation factor RRN7.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	410	Total	C	N	O	S	0	0
			3421	2219	579	603	20		

- Molecule 18 is a protein called RNA polymerase I-specific transcription initiation factor RRN11.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	R	303	Total	C	N	O	S	0	0
			2535	1634	456	434	11		

- Molecule 19 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
19	A	2	Total	Zn	0
			2	2	
19	B	1	Total	Zn	0
			1	1	
19	I	2	Total	Zn	0
			2	2	
19	J	1	Total	Zn	0
			1	1	

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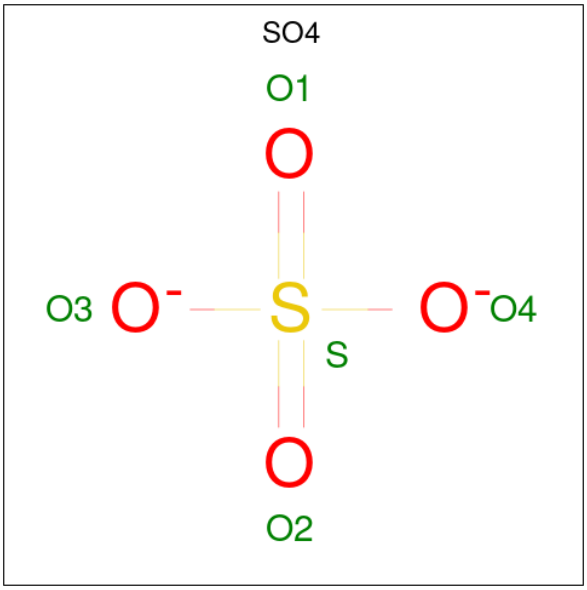
Mol	Chain	Residues	Atoms	AltConf
19	L	1	Total Zn 1 1	0
19	Q	1	Total Zn 1 1	0

- Molecule 20 is SULFATE ION (CCD ID: SO4) (formula: O_4S).



Mol	Chain	Residues	Atoms	AltConf
20	P	1	Total O S 5 4 1	0
20	P	1	Total O S 5 4 1	0
20	P	1	Total O S 5 4 1	0
20	Q	1	Total O S 5 4 1	0
20	R	1	Total O S 5 4 1	0

- Molecule 21 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

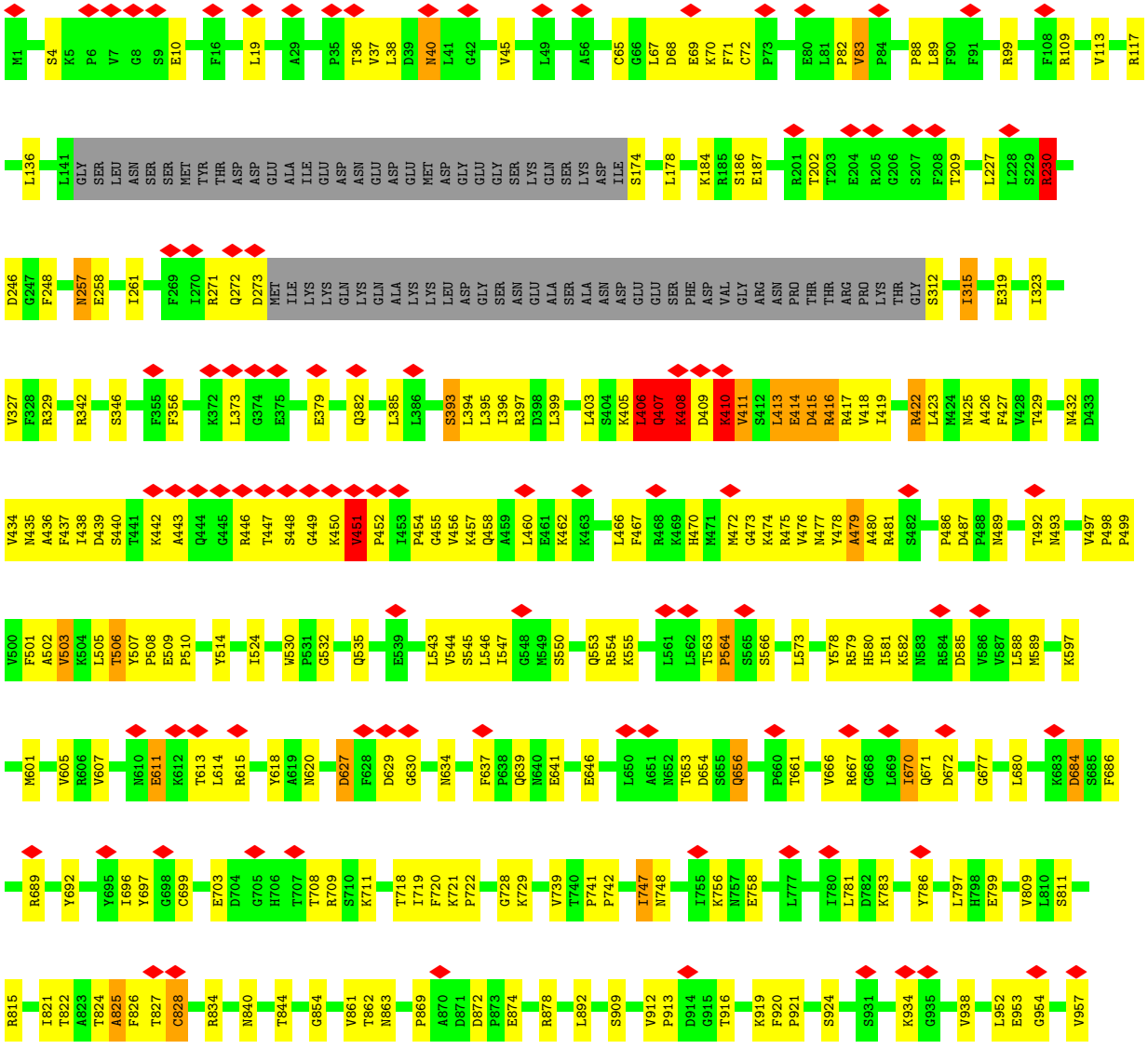
Mol	Chain	Residues	Atoms	AltConf
21	R	1	Total Mg 1 1	0

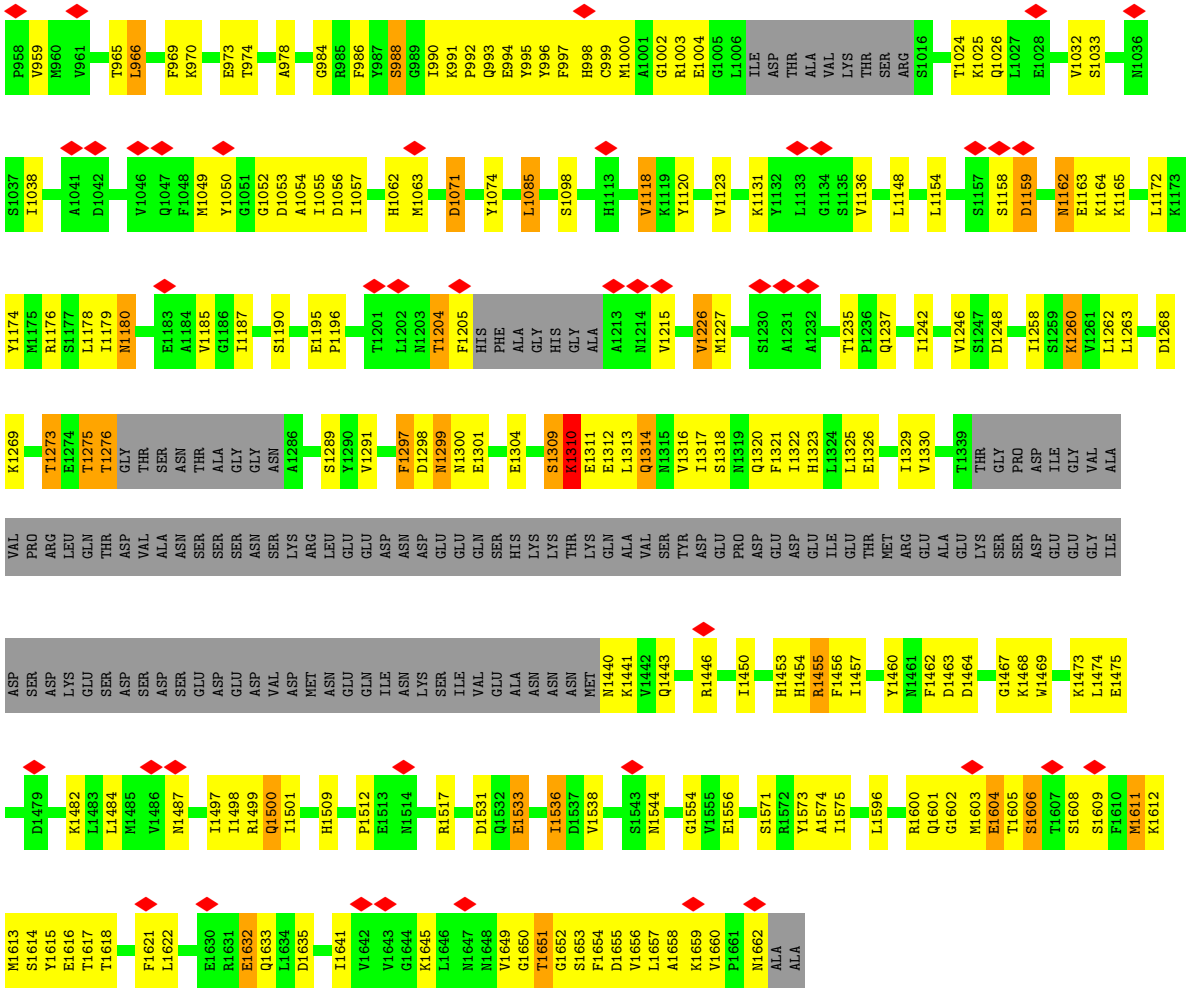
3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: DNA-directed RNA polymerase I subunit RPA190

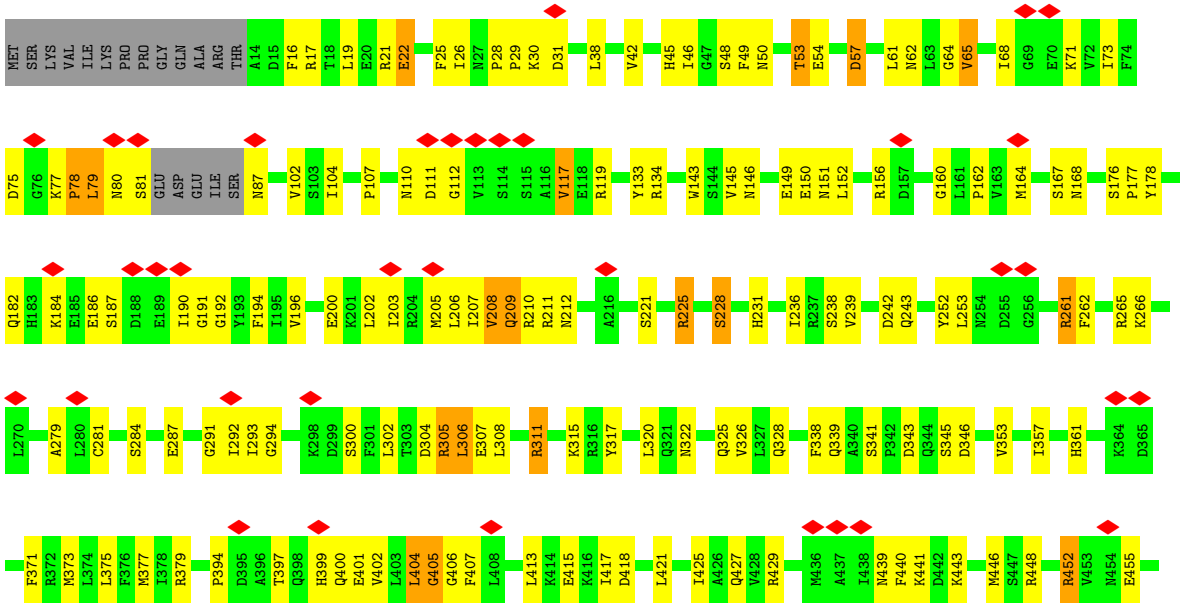
Chain A:

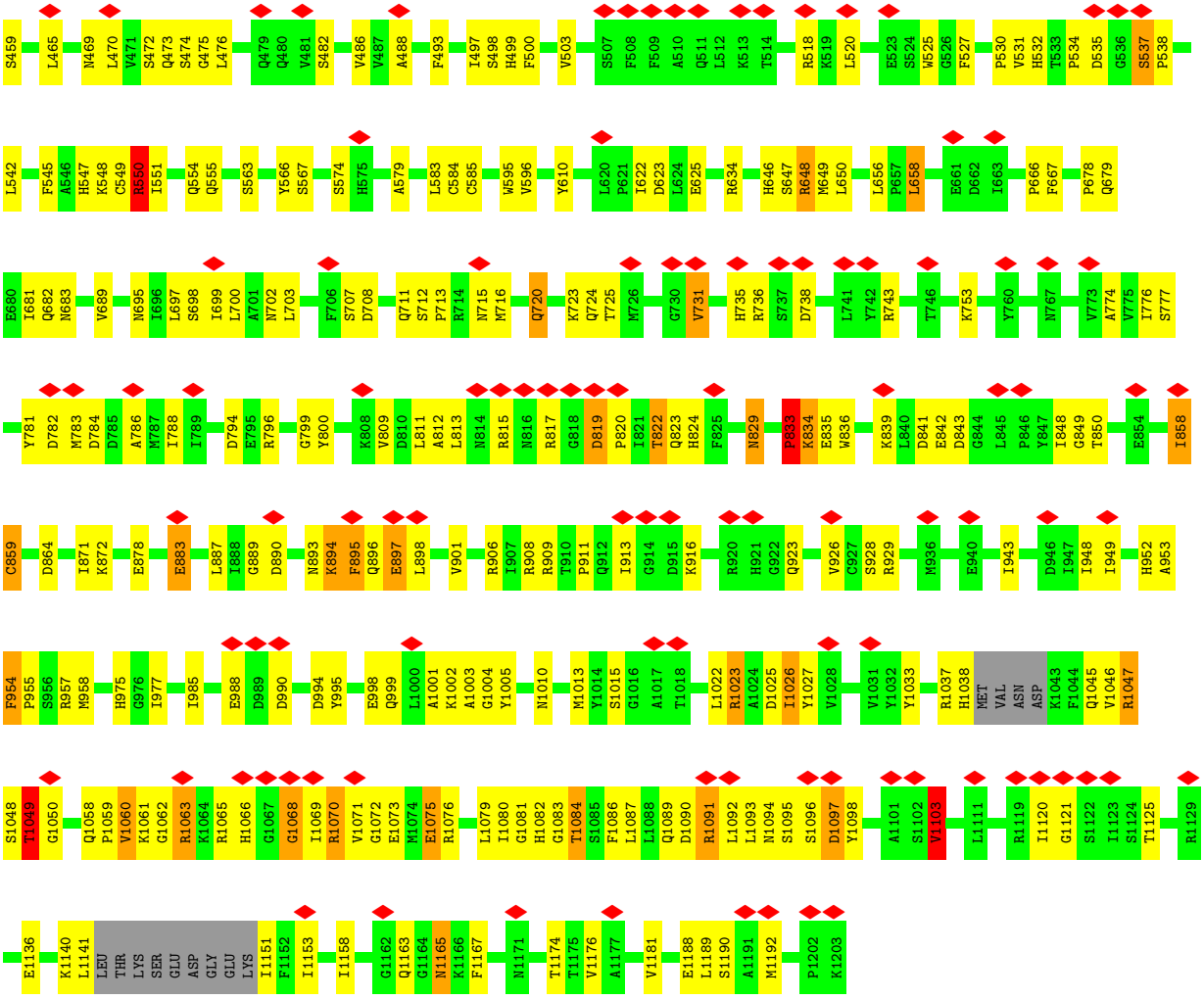




• Molecule 2: DNA-directed RNA polymerase I subunit RPA135

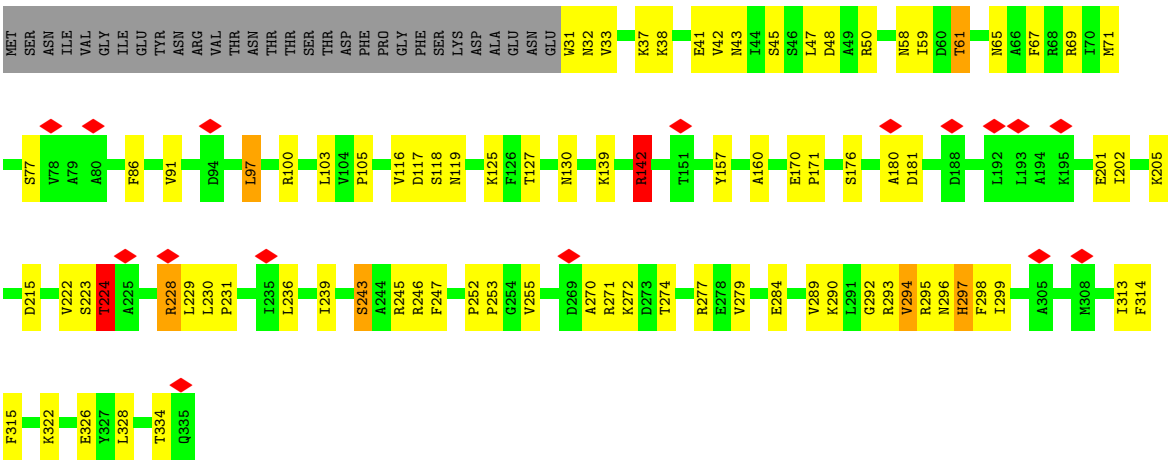
Chain B:





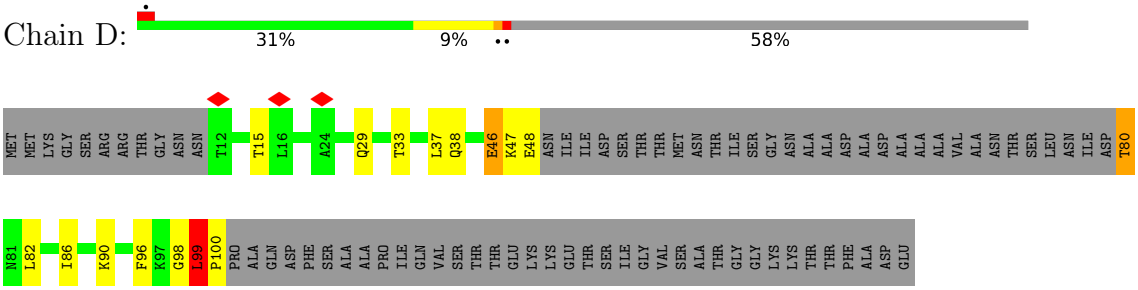
• Molecule 3: DNA-directed RNA polymerases I and III subunit RPAC1

Chain C:



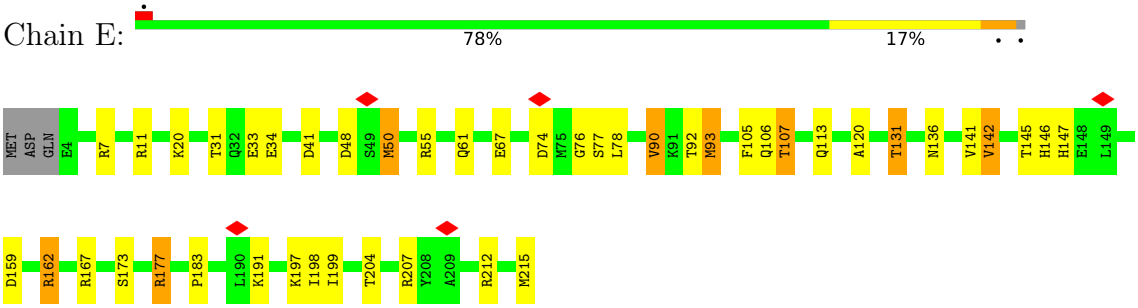
• Molecule 4: DNA-directed RNA polymerase I subunit RPA14

Chain D:



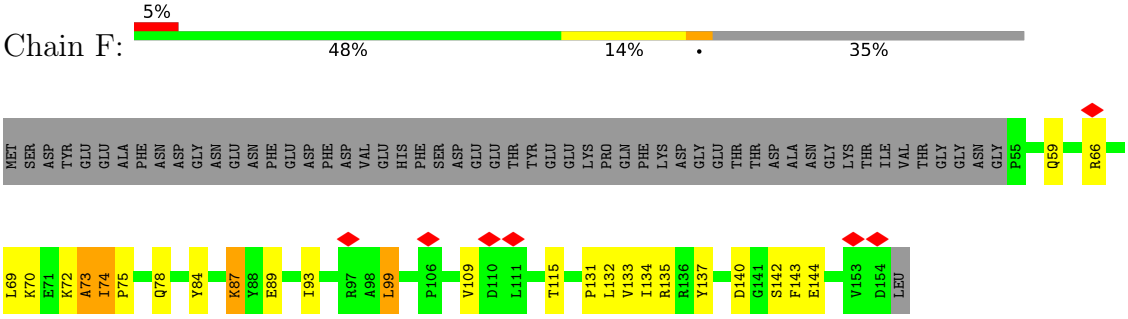
• Molecule 5: DNA-directed RNA polymerases I, II, and III subunit RPABC1

Chain E:



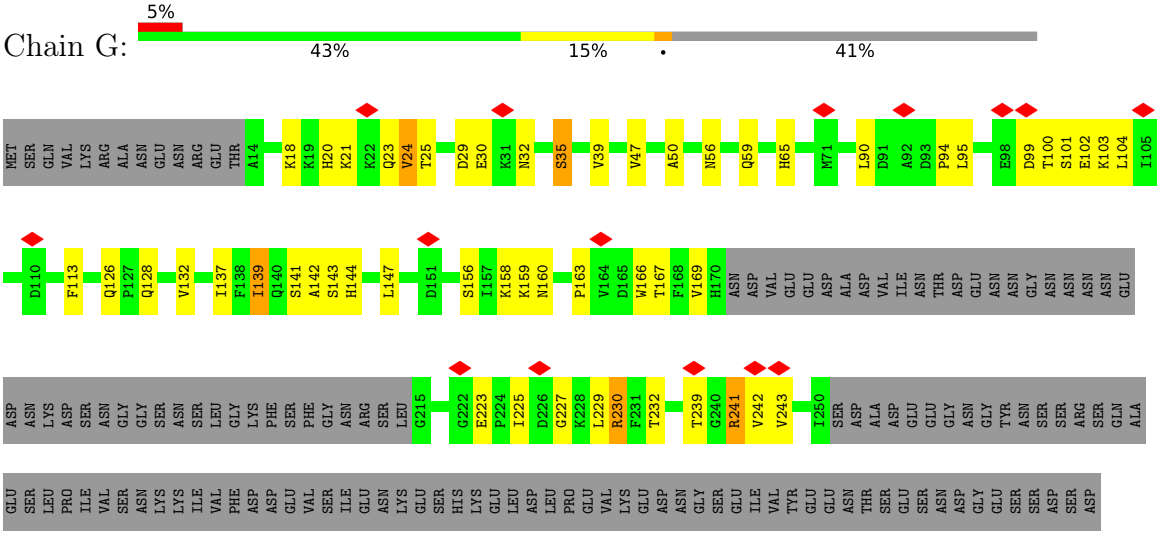
• Molecule 6: DNA-directed RNA polymerases I, II, and III subunit RPABC2

Chain F:



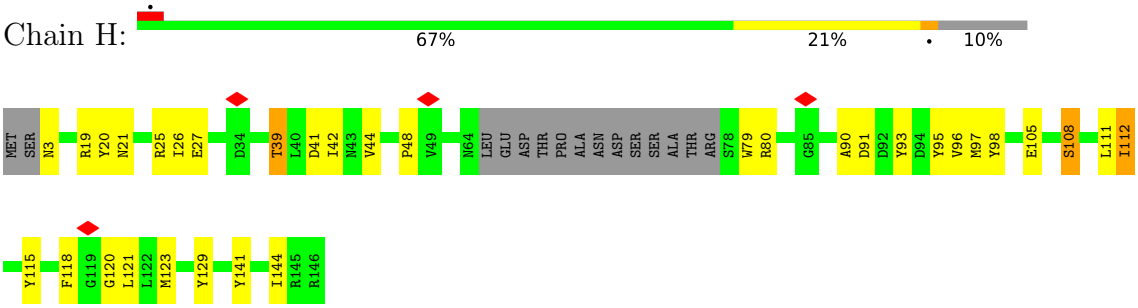
• Molecule 7: DNA-directed RNA polymerase I subunit RPA43

Chain G:



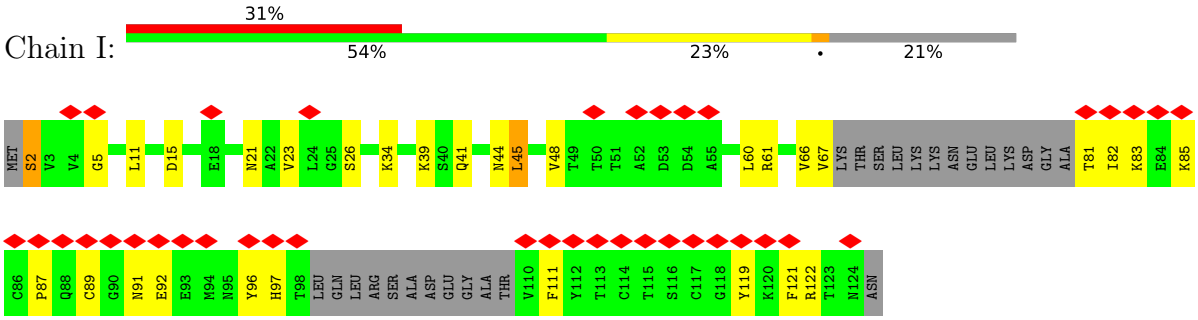
• Molecule 8: DNA-directed RNA polymerases I, II, and III subunit RPABC3

Chain H:



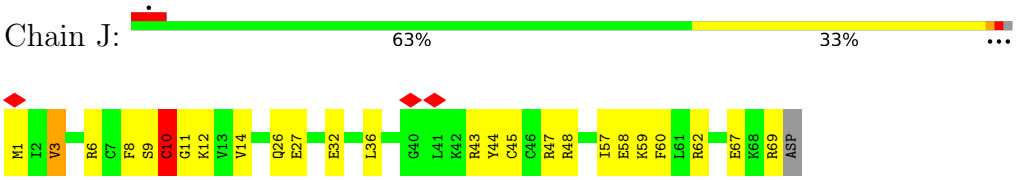
• Molecule 9: DNA-directed RNA polymerase I subunit RPA12

Chain I:



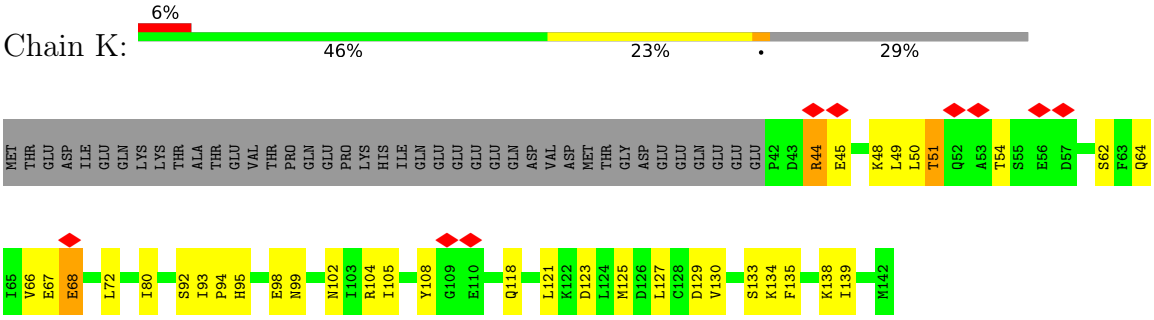
• Molecule 10: DNA-directed RNA polymerases I, II, and III subunit RPABC5

Chain J:



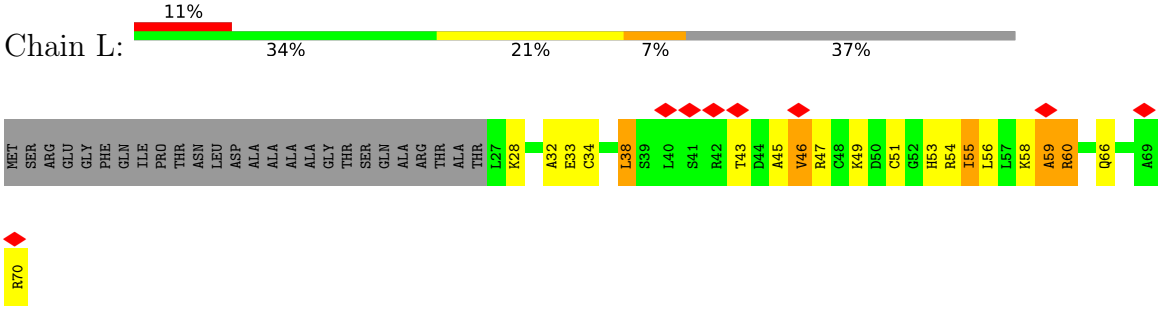
• Molecule 11: DNA-directed RNA polymerases I and III subunit RPAC2

Chain K:



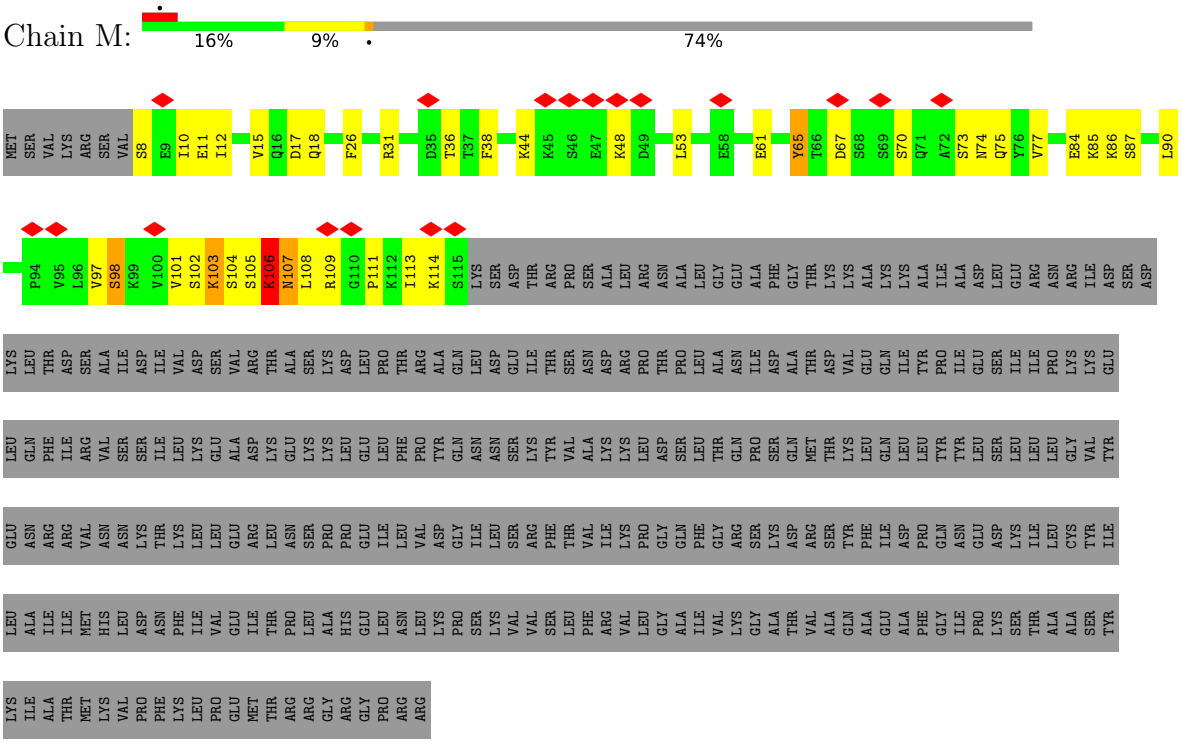
• Molecule 12: DNA-directed RNA polymerases I, II, and III subunit RPABC4

Chain L:



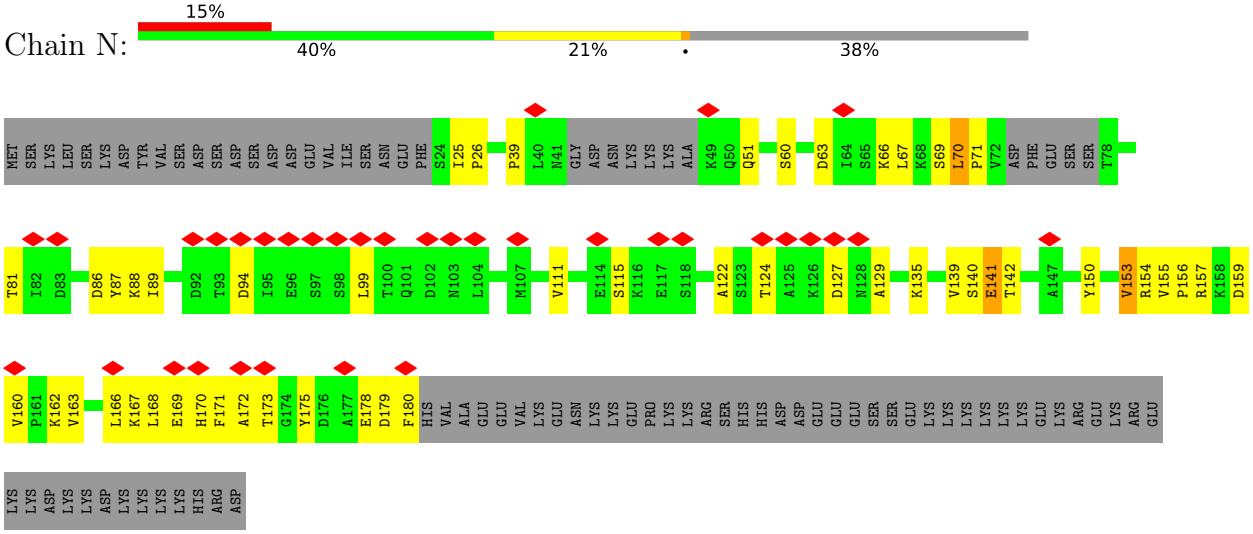
• Molecule 13: DNA-directed RNA polymerase I subunit RPA49

Chain M:



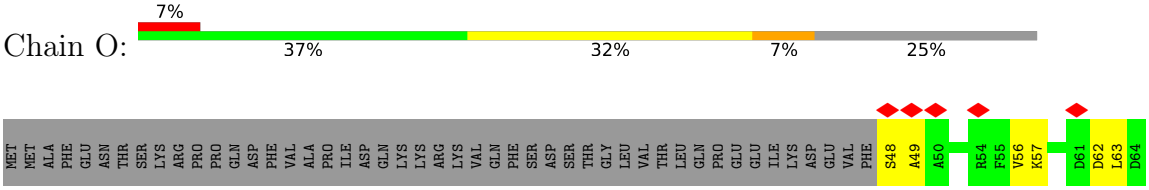
• Molecule 14: DNA-directed RNA polymerase I subunit RPA34

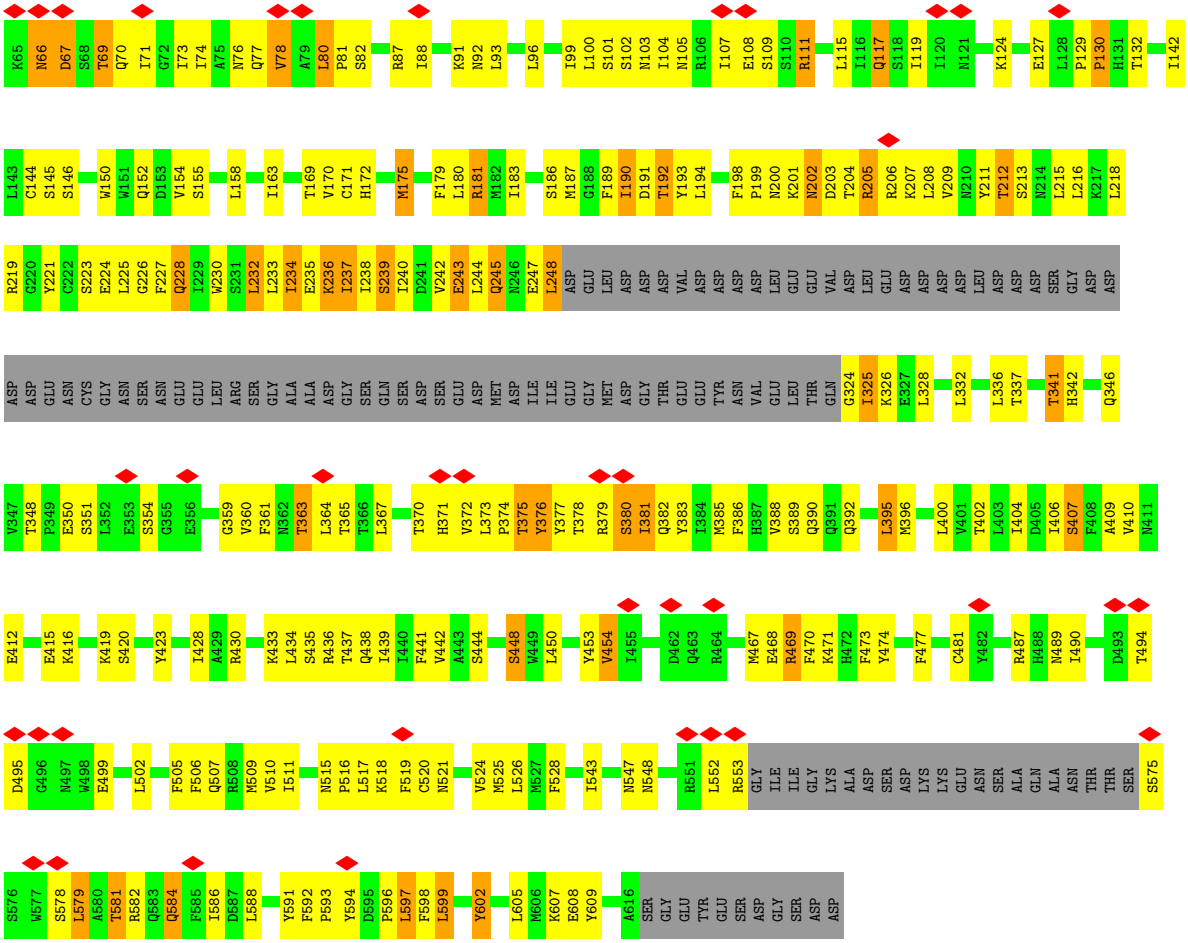
Chain N:



• Molecule 15: RNA polymerase I-specific transcription initiation factor RRN3

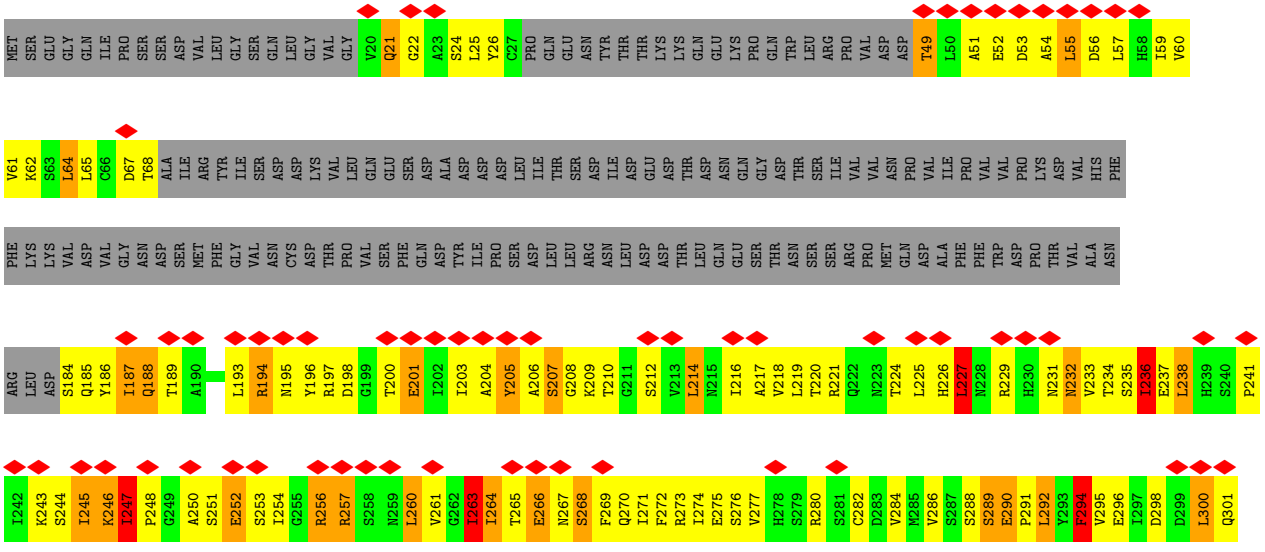
Chain O:



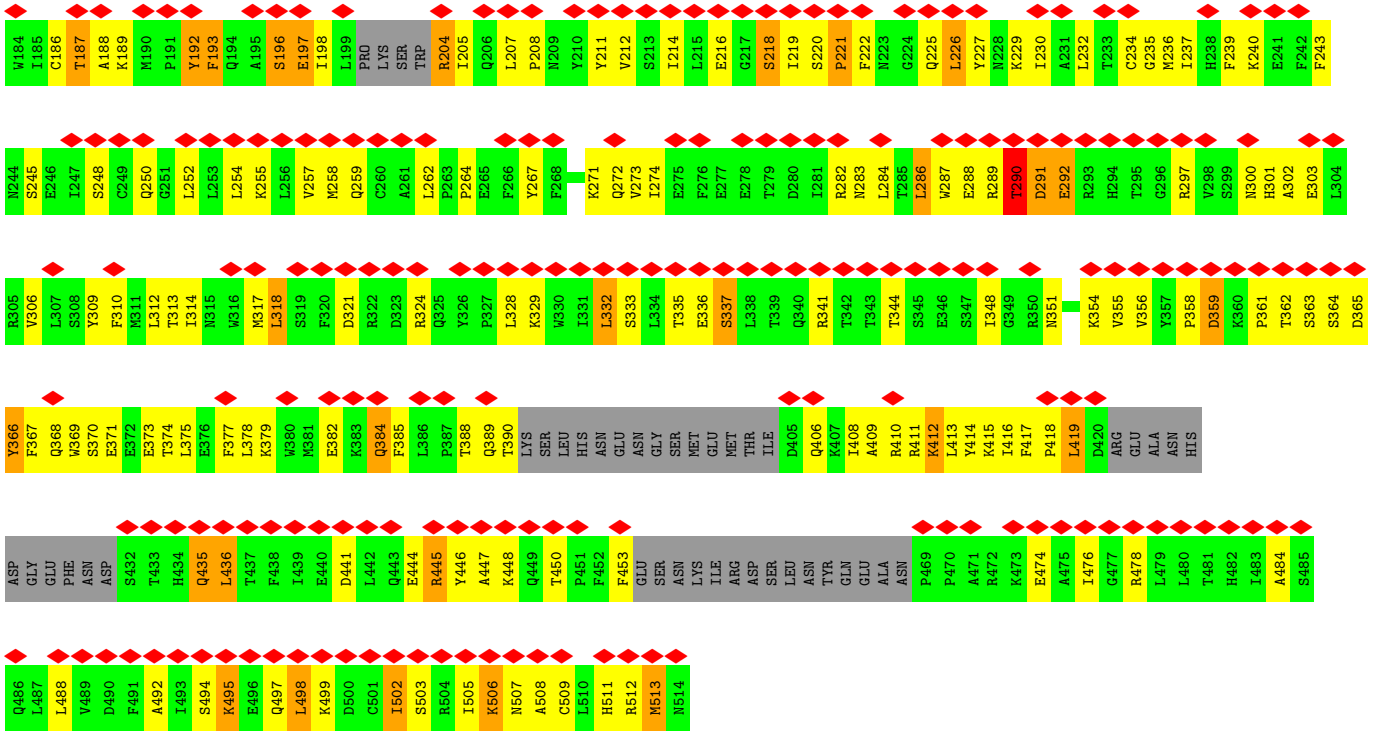


• Molecule 16: RNA polymerase I-specific transcription initiation factor RRN6

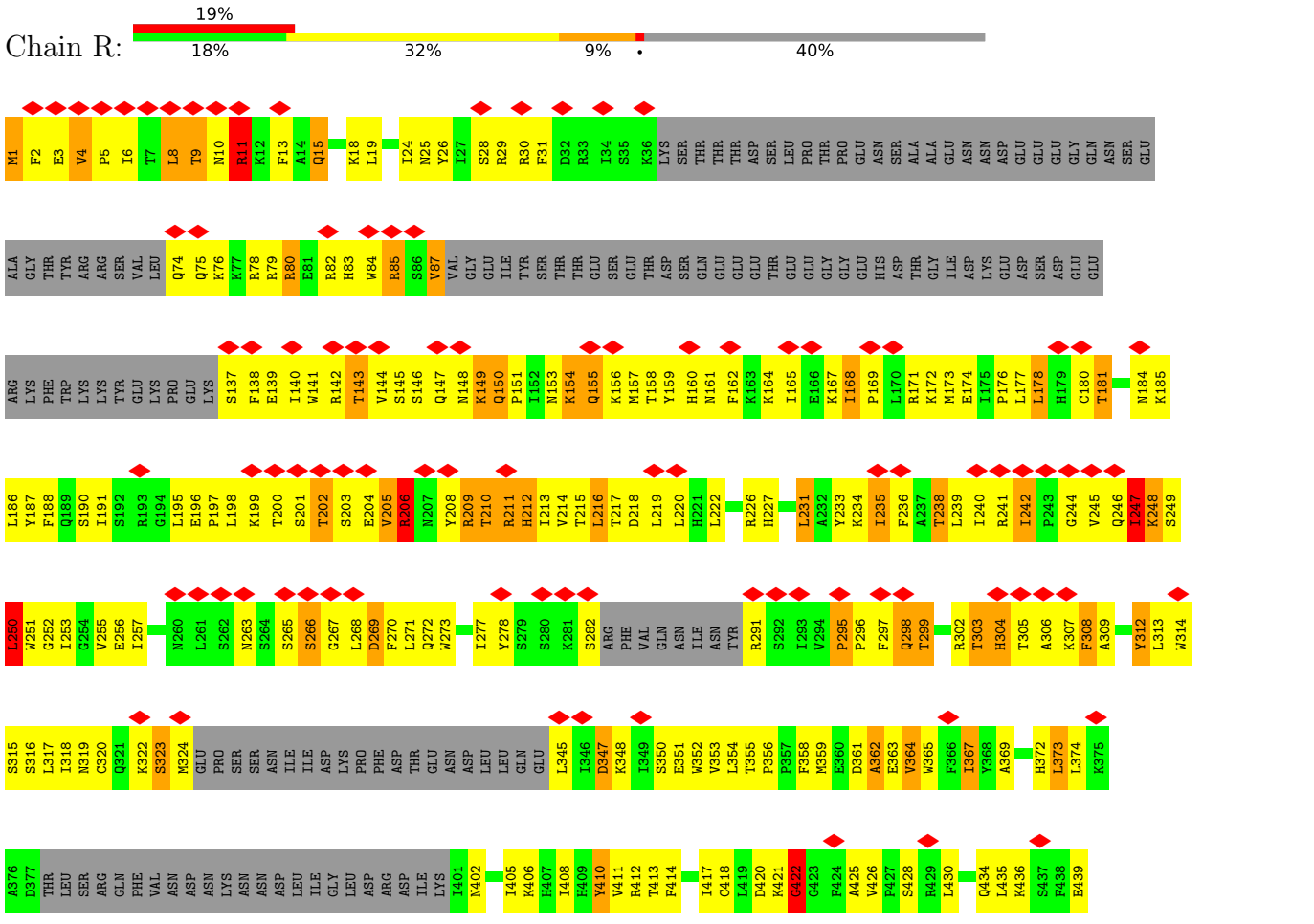
Chain P:

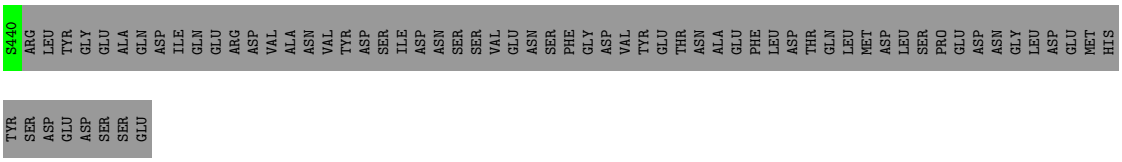


• Molecule 17: RNA polymerase I-specific transcription initiation factor RRN7



• Molecule 18: RNA polymerase I-specific transcription initiation factor RRN11




S440
ARG LEU TYR GLY GLU ALA GLN ASP ILE GLN GLU ARG ASP VAL ALA ASN VAL TYR ASP SER ILE ASP ASN SER SER VAL GLU ASN SER PHE GLY ASP VAL TYR GLU THR ASN ALA GLU PHE LEU ASP THR GLN LEU MET ASP LEU SER PRO GLU ASP ASN GLY LEU ASP GLU MET HIS
TYR SER ASP GLU ASP SER SER GLU

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	8317	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	40	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.068	Depositor
Minimum map value	-0.030	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.0205	Depositor
Map size (Å)	324.0, 324.0, 324.0	wwPDB
Map dimensions	240, 240, 240	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.35, 1.35, 1.35	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG, ZN, SO4

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|$ >5	RMSZ	#$\|Z\|$ >5
1	A	0.49	0/11809	0.72	20/15943 (0.1%)
2	B	0.50	2/9518 (0.0%)	0.78	26/12863 (0.2%)
3	C	0.42	0/2475	0.67	3/3354 (0.1%)
4	D	0.40	0/465	0.59	0/630
5	E	0.40	0/1771	0.66	3/2383 (0.1%)
6	F	0.45	0/838	0.58	0/1129
7	G	0.37	0/1563	0.66	3/2124 (0.1%)
8	H	0.42	0/1070	0.61	0/1449
9	I	0.44	0/765	0.58	0/1030
10	J	0.57	1/578 (0.2%)	0.59	0/775
11	K	0.46	0/804	0.79	3/1083 (0.3%)
12	L	0.42	0/354	0.60	0/468
13	M	0.40	0/872	0.55	0/1170
14	N	0.40	0/1172	0.54	0/1580
15	O	0.35	0/3996	0.54	0/5401
16	P	0.41	0/4822	0.68	4/6525 (0.1%)
17	Q	0.38	0/3502	0.64	2/4727 (0.0%)
18	R	0.37	0/2592	0.60	4/3486 (0.1%)
All	All	0.44	3/48966 (0.0%)	0.68	68/66120 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	15
2	B	0	4
3	C	0	1
6	F	0	1
12	L	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
13	M	0	3
14	N	0	1
15	O	0	4
16	P	0	26
17	Q	0	8
18	R	0	10
All	All	0	75

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	J	10	CYS	CB-SG	7.65	1.95	1.82
2	B	281	CYS	CB-SG	-6.94	1.70	1.82
2	B	859	CYS	CB-SG	-6.12	1.71	1.82

All (68) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
17	Q	7	GLY	C-N-CD	-15.27	87.00	120.60
2	B	1023	ARG	NE-CZ-NH2	-13.77	113.42	120.30
2	B	452	ARG	NE-CZ-NH2	-13.22	113.69	120.30
1	A	397	ARG	NE-CZ-NH1	13.12	126.86	120.30
2	B	448	ARG	NE-CZ-NH2	-13.05	113.77	120.30
1	A	329	ARG	NE-CZ-NH2	-12.95	113.82	120.30
1	A	329	ARG	NE-CZ-NH1	12.85	126.72	120.30
1	A	416	ARG	NE-CZ-NH2	-12.72	113.94	120.30
2	B	429	ARG	NE-CZ-NH2	-12.71	113.95	120.30
2	B	261	ARG	NE-CZ-NH1	12.51	126.56	120.30
2	B	448	ARG	NE-CZ-NH1	12.46	126.53	120.30
5	E	167	ARG	NE-CZ-NH2	-12.44	114.08	120.30
5	E	167	ARG	NE-CZ-NH1	12.38	126.49	120.30
11	K	44	ARG	NE-CZ-NH2	-12.24	114.18	120.30
2	B	452	ARG	NE-CZ-NH1	12.13	126.37	120.30
2	B	429	ARG	NE-CZ-NH1	12.08	126.34	120.30
2	B	634	ARG	NE-CZ-NH2	-12.07	114.26	120.30
2	B	261	ARG	NE-CZ-NH2	-12.07	114.27	120.30
11	K	44	ARG	NE-CZ-NH1	12.03	126.31	120.30
7	G	241	ARG	NE-CZ-NH2	-11.84	114.38	120.30
7	G	241	ARG	NE-CZ-NH1	11.78	126.19	120.30
1	A	397	ARG	NE-CZ-NH2	-11.69	114.45	120.30
1	A	422	ARG	NE-CZ-NH2	-11.51	114.55	120.30
3	C	142	ARG	NE-CZ-NH2	-11.38	114.61	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	C	142	ARG	NE-CZ-NH1	11.30	125.95	120.30
1	A	422	ARG	NE-CZ-NH1	11.29	125.94	120.30
1	A	416	ARG	NE-CZ-NH1	11.22	125.91	120.30
1	A	342	ARG	NE-CZ-NH2	-11.18	114.71	120.30
2	B	634	ARG	NE-CZ-NH1	11.03	125.81	120.30
2	B	550	ARG	NE-CZ-NH2	-10.81	114.90	120.30
1	A	230	ARG	NE-CZ-NH1	10.71	125.65	120.30
2	B	648	ARG	NE-CZ-NH2	-10.71	114.95	120.30
1	A	230	ARG	NE-CZ-NH2	-10.70	114.95	120.30
2	B	550	ARG	NE-CZ-NH1	10.07	125.33	120.30
2	B	1023	ARG	NE-CZ-NH1	9.52	125.06	120.30
1	A	342	ARG	NE-CZ-NH1	9.11	124.86	120.30
2	B	648	ARG	NE-CZ-NH1	9.09	124.84	120.30
18	R	250	LEU	CA-CB-CG	8.90	135.78	115.30
1	A	397	ARG	CD-NE-CZ	6.96	133.34	123.60
2	B	261	ARG	CD-NE-CZ	6.89	133.25	123.60
2	B	452	ARG	CD-NE-CZ	6.58	132.81	123.60
1	A	329	ARG	CD-NE-CZ	6.39	132.55	123.60
2	B	405	GLY	N-CA-C	-6.36	97.20	113.10
18	R	205	VAL	N-CA-C	6.35	128.15	111.00
2	B	448	ARG	CD-NE-CZ	6.31	132.43	123.60
2	B	634	ARG	CD-NE-CZ	6.24	132.34	123.60
11	K	44	ARG	CD-NE-CZ	6.23	132.32	123.60
1	A	422	ARG	CD-NE-CZ	6.20	132.28	123.60
17	Q	119	LEU	CA-CB-CG	6.17	129.48	115.30
1	A	416	ARG	CD-NE-CZ	6.16	132.23	123.60
2	B	429	ARG	CD-NE-CZ	6.16	132.23	123.60
16	P	463	LEU	CA-CB-CG	6.14	129.43	115.30
16	P	227	LEU	CA-CB-CG	6.11	129.34	115.30
3	C	142	ARG	CD-NE-CZ	6.02	132.02	123.60
7	G	241	ARG	CD-NE-CZ	5.96	131.95	123.60
5	E	167	ARG	CD-NE-CZ	5.95	131.93	123.60
1	A	356	PHE	O-C-N	-5.92	113.22	122.70
1	A	342	ARG	CD-NE-CZ	5.74	131.63	123.60
18	R	206	ARG	N-CA-C	5.73	126.46	111.00
2	B	1103	VAL	CB-CA-C	-5.63	100.70	111.40
2	B	550	ARG	CD-NE-CZ	5.41	131.17	123.60
2	B	648	ARG	CD-NE-CZ	5.38	131.13	123.60
2	B	1023	ARG	CD-NE-CZ	5.25	130.95	123.60
1	A	230	ARG	CD-NE-CZ	5.21	130.90	123.60
16	P	343	LEU	CA-CB-CG	5.21	127.28	115.30
18	R	178	LEU	CA-CB-CG	5.11	127.05	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
16	P	663	LEU	CA-CB-CG	5.05	126.92	115.30
1	A	1071	ASP	N-CA-C	-5.00	97.50	111.00

There are no chirality outliers.

All (75) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1180	ASN	Peptide
1	A	1260	LYS	Peptide
1	A	1297	PHE	Peptide
1	A	1309	SER	Peptide
1	A	1310	LYS	Peptide
1	A	1649	VAL	Peptide
1	A	405	LYS	Peptide
1	A	406	LEU	Peptide
1	A	407	GLN	Peptide
1	A	410	LYS	Peptide
1	A	411	VAL	Peptide
1	A	506	THR	Peptide
1	A	781	LEU	Peptide
1	A	825	ALA	Peptide
1	A	828	CYS	Peptide
2	B	1049	THR	Peptide
2	B	1068	GLY	Peptide
2	B	404	LEU	Peptide
2	B	550	ARG	Peptide
3	C	294	VAL	Peptide
6	F	73	ALA	Peptide
12	L	59	ALA	Peptide
12	L	60	ARG	Peptide
13	M	103	LYS	Peptide
13	M	106	LYS	Peptide
13	M	107	ASN	Peptide
14	N	141	GLU	Peptide
15	O	236	LYS	Peptide
15	O	243	GLU	Peptide
15	O	375	THR	Peptide
15	O	380	SER	Peptide
16	P	216	ILE	Peptide
16	P	236	ILE	Peptide
16	P	238	LEU	Peptide
16	P	247	ILE	Peptide

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Mol	Chain	Res	Type	Group
16	P	256	ARG	Peptide
16	P	260	LEU	Peptide
16	P	263	ILE	Peptide
16	P	270	GLN	Peptide
16	P	289	SER	Peptide
16	P	294	PHE	Peptide
16	P	295	VAL	Peptide
16	P	333	PHE	Peptide
16	P	365	TRP	Peptide
16	P	393	VAL	Peptide
16	P	408	ILE	Peptide
16	P	433	VAL	Peptide
16	P	442	LEU	Peptide
16	P	485	LYS	Peptide
16	P	500	ILE	Peptide
16	P	51	ALA	Peptide
16	P	52	GLU	Peptide
16	P	580	ASN	Peptide
16	P	661	ASN	Peptide
16	P	667	ASP	Peptide
16	P	767	PRO	Peptide
16	P	769	GLN	Peptide
17	Q	148	PRO	Peptide
17	Q	15	CYS	Peptide
17	Q	17	SER	Peptide
17	Q	221	PRO	Peptide
17	Q	25	GLY	Peptide
17	Q	29	CYS	Peptide
17	Q	290	THR	Peptide
17	Q	4	PHE	Peptide
18	R	154	LYS	Peptide
18	R	206	ARG	Peptide
18	R	247	ILE	Peptide
18	R	263	ASN	Peptide
18	R	265	SER	Peptide
18	R	303	THR	Peptide
18	R	304	HIS	Peptide
18	R	422	GLY	Peptide
18	R	425	ALA	Peptide
18	R	9	THR	Peptide

5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	11598	0	11666	1168	0
2	B	9312	0	9200	980	0
3	C	2423	0	2412	139	0
4	D	459	0	462	8	0
5	E	1735	0	1764	30	0
6	F	823	0	839	96	0
7	G	1526	0	1534	151	0
8	H	1052	0	1021	55	0
9	I	755	0	728	104	0
10	J	569	0	584	55	0
11	K	793	0	790	54	0
12	L	352	0	371	58	0
13	M	856	0	852	59	0
14	N	1151	0	1168	166	0
15	O	3907	0	3902	406	0
16	P	4729	0	4670	579	0
17	Q	3421	0	3463	446	0
18	R	2535	0	2606	599	0
19	A	2	0	0	1	0
19	B	1	0	0	0	0
19	I	2	0	0	0	0
19	J	1	0	0	0	0
19	L	1	0	0	0	0
19	Q	1	0	0	0	0
20	P	15	0	0	2	0
20	Q	5	0	0	1	0
20	R	5	0	0	4	0
21	R	1	0	0	0	0
All	All	48030	0	48032	3777	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 39.

All (3777) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:272:LYS:HA	14:N:175:TYR:CE1	1.16	1.69
1:A:990:ILE:CB	1:A:994:GLU:HB2	1.19	1.66
1:A:995:TYR:CD2	2:B:708:ASP:HA	1.29	1.65
16:P:473:HIS:CD2	18:R:1:MET:HB2	1.16	1.63
17:Q:20:TRP:CZ3	17:Q:22:ILE:CG2	1.76	1.62
15:O:248:LEU:HD12	15:O:598:PHE:CD2	1.32	1.61
17:Q:12:THR:HG21	17:Q:33:HIS:CE1	1.12	1.60
17:Q:20:TRP:HZ3	17:Q:22:ILE:CG2	1.10	1.60
6:F:72:LYS:HB3	6:F:142:SER:CA	1.30	1.59
1:A:545:SER:HB2	17:Q:34:VAL:CG2	1.14	1.59
13:M:102:SER:HB3	13:M:105:SER:CB	1.28	1.58
17:Q:12:THR:CG2	17:Q:33:HIS:HE1	1.10	1.58
15:O:200:ASN:HB2	17:Q:14:ASN:CB	1.34	1.57
18:R:5:PRO:HG2	18:R:217:THR:CG2	1.16	1.57
1:A:1322:ILE:HG22	1:A:1454:HIS:CD2	1.37	1.57
1:A:1484:LEU:HD13	2:B:305:ARG:CZ	1.24	1.56
7:G:143:SER:HB2	15:O:104:ILE:CG2	1.36	1.55
2:B:152:LEU:CB	2:B:443:LYS:HE3	1.37	1.55
1:A:1575:ILE:CG1	9:I:122:ARG:NH1	1.68	1.54
7:G:143:SER:CB	15:O:104:ILE:HG22	1.33	1.53
2:B:152:LEU:HB3	2:B:443:LYS:CE	1.34	1.53
15:O:200:ASN:CB	17:Q:14:ASN:HB2	1.07	1.53
15:O:248:LEU:CD1	15:O:598:PHE:CD2	1.92	1.52
1:A:990:ILE:HB	1:A:994:GLU:CB	1.06	1.52
15:O:248:LEU:CD1	15:O:598:PHE:CE2	1.93	1.51
2:B:679:GLN:CG	14:N:157:ARG:N	1.75	1.50
16:P:473:HIS:HD2	18:R:1:MET:CB	1.19	1.50
15:O:200:ASN:CG	17:Q:14:ASN:HB2	1.30	1.49
15:O:248:LEU:HD12	15:O:598:PHE:CE2	0.97	1.49
1:A:545:SER:CB	17:Q:34:VAL:HG21	1.01	1.49
2:B:527:PHE:CD1	2:B:666:PRO:HG3	1.47	1.49
3:C:272:LYS:CA	14:N:175:TYR:CE1	1.92	1.48
3:C:253:PRO:CD	14:N:180:PHE:HB3	1.09	1.48
1:A:547:ILE:CD1	17:Q:26:ARG:NH1	1.68	1.48
6:F:72:LYS:CD	6:F:142:SER:HB3	1.43	1.48
2:B:143:TRP:HB2	2:B:446:MET:CE	1.43	1.47
2:B:527:PHE:CZ	2:B:666:PRO:HA	1.49	1.47
2:B:207:ILE:HG13	2:B:503:VAL:CG2	1.41	1.47
1:A:1049:MET:HG2	1:A:1052:GLY:C	1.30	1.46
18:R:5:PRO:CG	18:R:217:THR:CB	1.92	1.46
18:R:251:TRP:CE3	18:R:307:LYS:HE3	1.50	1.46
1:A:547:ILE:HD11	17:Q:26:ARG:NH1	1.18	1.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:848:ILE:CB	12:L:60:ARG:HD2	1.46	1.45
17:Q:358:PRO:CA	18:R:206:ARG:HH12	1.29	1.45
3:C:58:ASN:HA	3:C:296:ASN:ND2	1.18	1.44
7:G:141:SER:HB3	15:O:142:ILE:CD1	1.46	1.44
2:B:68:ILE:HG21	2:B:71:LYS:NZ	1.32	1.43
2:B:1089:GLN:CG	2:B:1093:LEU:HD22	1.46	1.43
18:R:5:PRO:CG	18:R:217:THR:HB	1.44	1.43
14:N:87:TYR:CA	14:N:141:GLU:HA	1.48	1.43
1:A:597:LYS:HB2	2:B:1082:HIS:NE2	1.23	1.42
1:A:878:ARG:HB3	9:I:67:VAL:CG1	1.47	1.42
18:R:251:TRP:CE3	18:R:307:LYS:CE	2.01	1.42
1:A:1297:PHE:CE2	1:A:1301:GLU:OE1	1.70	1.41
16:P:436:ILE:HG22	18:R:142:ARG:C	1.07	1.41
1:A:429:THR:HG21	18:R:406:LYS:CE	1.50	1.41
3:C:272:LYS:HA	14:N:175:TYR:CZ	1.51	1.41
16:P:397:LYS:HZ1	18:R:85:ARG:NH1	1.18	1.41
1:A:756:LYS:CD	9:I:85:LYS:NZ	1.79	1.41
7:G:159:LYS:H	15:O:105:ASN:ND2	0.91	1.41
6:F:72:LYS:CB	6:F:142:SER:HA	1.50	1.40
15:O:240:ILE:HG22	15:O:380:SER:CB	1.48	1.40
2:B:143:TRP:CE3	2:B:446:MET:HG3	1.57	1.40
1:A:597:LYS:HB2	2:B:1082:HIS:CD2	1.58	1.38
3:C:253:PRO:HD2	14:N:180:PHE:CB	1.31	1.38
2:B:207:ILE:CG1	2:B:503:VAL:HG21	1.49	1.38
2:B:679:GLN:CG	14:N:156:PRO:C	1.92	1.38
13:M:102:SER:CB	13:M:105:SER:HB3	1.13	1.38
16:P:397:LYS:HE2	18:R:85:ARG:NE	1.38	1.38
1:A:1326:GLU:CD	1:A:1455:ARG:N	1.76	1.38
1:A:1322:ILE:HD12	1:A:1457:ILE:CD1	1.53	1.37
7:G:141:SER:CB	15:O:142:ILE:HD12	1.54	1.37
16:P:397:LYS:HZ1	18:R:85:ARG:CZ	1.36	1.37
16:P:436:ILE:CG2	18:R:142:ARG:O	1.72	1.37
1:A:629:ASP:C	2:B:926:VAL:HG21	1.42	1.36
6:F:74:ILE:O	7:G:95:LEU:CD1	1.69	1.36
7:G:159:LYS:N	15:O:105:ASN:ND2	1.70	1.36
1:A:1322:ILE:CG2	1:A:1454:HIS:CG	2.08	1.35
18:R:5:PRO:CG	18:R:217:THR:CG2	2.01	1.35
15:O:200:ASN:CB	17:Q:14:ASN:CB	1.95	1.35
17:Q:351:ASN:HB3	17:Q:369:TRP:CH2	1.61	1.35
1:A:999:CYS:HA	2:B:712:SER:CB	1.54	1.34
16:P:397:LYS:CE	18:R:85:ARG:NE	1.90	1.34

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:547:ILE:HD12	17:Q:26:ARG:CZ	1.53	1.34
2:B:743:ARG:NH2	10:J:60:PHE:CZ	1.96	1.34
2:B:143:TRP:CG	2:B:446:MET:SD	2.21	1.34
2:B:848:ILE:HB	12:L:60:ARG:CD	1.56	1.34
15:O:234:ILE:CG2	15:O:237:ILE:HG12	1.41	1.34
2:B:143:TRP:CB	2:B:446:MET:HE3	1.55	1.34
2:B:1002:LYS:HD3	14:N:166:LEU:O	1.16	1.34
7:G:141:SER:CB	15:O:142:ILE:CD1	2.06	1.34
17:Q:356:VAL:HG11	18:R:208:TYR:CD1	1.62	1.34
2:B:796:ARG:NE	10:J:8:PHE:O	1.58	1.33
1:A:1276:THR:OG1	9:I:45:LEU:HD12	1.22	1.33
1:A:1482:LYS:CE	2:B:304:ASP:OD1	1.74	1.33
18:R:199:LYS:HE3	20:R:601:SO4:O2	1.27	1.33
1:A:1326:GLU:OE2	1:A:1454:HIS:HB3	1.26	1.32
16:P:397:LYS:NZ	18:R:85:ARG:NH1	1.74	1.32
1:A:503:VAL:HA	1:A:580:HIS:CD2	1.61	1.32
1:A:1297:PHE:CD2	1:A:1301:GLU:OE1	1.81	1.32
1:A:545:SER:CB	17:Q:34:VAL:CG2	1.77	1.32
2:B:68:ILE:CG2	2:B:71:LYS:NZ	1.91	1.32
7:G:159:LYS:CB	15:O:105:ASN:HD22	1.43	1.32
2:B:549:CYS:SG	2:B:649:MET:HG2	1.70	1.31
1:A:1326:GLU:OE2	1:A:1455:ARG:N	1.60	1.31
2:B:143:TRP:CD2	2:B:446:MET:HG3	1.65	1.31
2:B:322:ASN:ND2	13:M:108:LEU:O	1.57	1.31
2:B:890:ASP:O	12:L:54:ARG:HD3	1.24	1.31
1:A:547:ILE:CD1	17:Q:26:ARG:CZ	2.08	1.31
1:A:1322:ILE:HG22	1:A:1454:HIS:CG	1.62	1.31
17:Q:26:ARG:HB3	17:Q:34:VAL:CG1	1.61	1.31
1:A:1299:ASN:OD1	1:A:1467:GLY:CA	1.71	1.30
3:C:272:LYS:HA	14:N:175:TYR:CD1	1.63	1.30
7:G:24:VAL:O	7:G:128:GLN:HB2	1.17	1.30
1:A:990:ILE:HA	1:A:994:GLU:OE1	1.30	1.30
2:B:19:LEU:CD1	10:J:26:GLN:OE1	1.78	1.30
1:A:1276:THR:OG1	9:I:45:LEU:CD1	1.79	1.30
1:A:535:GLN:NE2	17:Q:26:ARG:HD3	1.43	1.30
2:B:527:PHE:CZ	2:B:666:PRO:CA	2.13	1.30
18:R:15:GLN:OE1	18:R:184:ASN:ND2	1.63	1.30
16:P:390:GLN:CB	18:R:150:GLN:O	1.78	1.29
1:A:547:ILE:HD12	17:Q:26:ARG:NH2	1.46	1.29
2:B:1003:ALA:O	14:N:170:HIS:N	1.66	1.29
16:P:436:ILE:HG22	18:R:142:ARG:O	1.23	1.29

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:756:LYS:HD3	9:I:85:LYS:NZ	0.97	1.28
16:P:198:ASP:CB	16:P:205:TYR:O	1.79	1.28
16:P:397:LYS:NZ	18:R:85:ARG:CZ	1.94	1.28
18:R:177:LEU:O	18:R:185:LYS:HE2	1.13	1.28
18:R:199:LYS:HE2	18:R:204:GLU:CA	1.61	1.28
13:M:102:SER:O	13:M:106:LYS:N	1.66	1.28
1:A:995:TYR:OH	2:B:707:SER:CB	1.79	1.27
2:B:75:ASP:HB3	2:B:440:PHE:CE2	1.67	1.27
2:B:527:PHE:CE1	2:B:666:PRO:HG3	1.69	1.27
2:B:679:GLN:HG2	14:N:157:ARG:N	0.96	1.27
17:Q:12:THR:CG2	17:Q:33:HIS:CE1	1.95	1.27
17:Q:20:TRP:CZ3	17:Q:22:ILE:HG23	1.48	1.27
16:P:198:ASP:HB2	16:P:205:TYR:O	1.27	1.27
1:A:435:ASN:HB3	1:A:442:LYS:CB	1.64	1.27
3:C:253:PRO:HD2	14:N:180:PHE:CG	1.68	1.27
2:B:682:GLN:CA	14:N:154:ARG:HH21	1.46	1.26
16:P:433:VAL:HA	18:R:145:SER:OG	1.24	1.26
2:B:1072:GLY:C	2:B:1075:GLU:HG2	1.55	1.26
1:A:990:ILE:HG13	1:A:995:TYR:N	1.47	1.26
2:B:1072:GLY:O	2:B:1075:GLU:HG2	1.26	1.26
7:G:159:LYS:HD2	15:O:103:ASN:OD1	1.09	1.26
18:R:199:LYS:CE	18:R:204:GLU:HB3	1.65	1.26
2:B:683:ASN:N	14:N:154:ARG:NH2	1.84	1.26
17:Q:358:PRO:HA	18:R:206:ARG:NH1	1.51	1.25
15:O:247:GLU:OE1	15:O:325:ILE:CG1	1.85	1.25
18:R:199:LYS:HE2	18:R:204:GLU:CB	1.64	1.25
16:P:397:LYS:CE	18:R:85:ARG:CZ	2.14	1.25
1:A:878:ARG:CG	9:I:66:VAL:HG23	1.65	1.25
1:A:1330:VAL:HG21	1:A:1455:ARG:CZ	1.66	1.25
2:B:682:GLN:C	14:N:154:ARG:HH21	1.37	1.25
14:N:86:ASP:C	14:N:141:GLU:HG3	1.58	1.24
17:Q:351:ASN:CB	17:Q:369:TRP:CH2	2.20	1.24
2:B:1089:GLN:HG3	2:B:1093:LEU:CG	1.65	1.24
16:P:436:ILE:CG2	18:R:142:ARG:C	2.02	1.24
15:O:200:ASN:CG	17:Q:14:ASN:CB	2.05	1.24
1:A:1322:ILE:CG2	1:A:1454:HIS:CD2	2.19	1.24
2:B:207:ILE:CG1	2:B:503:VAL:CG2	2.07	1.24
16:P:397:LYS:NZ	18:R:85:ARG:CD	2.00	1.23
1:A:1180:ASN:OD1	6:F:87:LYS:HD3	1.33	1.23
14:N:87:TYR:HA	14:N:141:GLU:CA	1.69	1.23
15:O:376:TYR:CE2	15:O:377:TYR:CE2	2.24	1.23

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1322:ILE:HG21	1:A:1454:HIS:ND1	1.54	1.22
1:A:1650:GLY:O	1:A:1652:GLY:N	1.73	1.22
14:N:86:ASP:O	14:N:141:GLU:HG3	1.37	1.22
1:A:403:LEU:HD11	1:A:419:ILE:CG2	1.68	1.22
1:A:545:SER:CA	17:Q:34:VAL:HG21	1.70	1.22
16:P:443:ASP:O	18:R:3:GLU:HB2	1.31	1.22
1:A:458:GLN:O	1:A:462:LYS:HB2	1.36	1.22
1:A:1326:GLU:CD	1:A:1454:HIS:HB3	1.57	1.22
2:B:682:GLN:C	14:N:154:ARG:NH2	1.91	1.22
1:A:1484:LEU:CD1	2:B:305:ARG:CZ	2.17	1.21
1:A:1575:ILE:HG13	9:I:122:ARG:CZ	1.70	1.21
14:N:86:ASP:O	14:N:141:GLU:CG	1.88	1.21
18:R:6:ILE:HD11	18:R:213:ILE:CG2	1.70	1.21
2:B:68:ILE:CG2	2:B:71:LYS:HZ3	1.51	1.21
1:A:474:LYS:NZ	2:B:1096:SER:OG	1.74	1.21
2:B:182:GLN:NE2	10:J:69:ARG:HB3	1.55	1.21
1:A:991:LYS:N	1:A:994:GLU:HG3	1.54	1.21
2:B:679:GLN:HG3	14:N:156:PRO:C	1.55	1.21
13:M:61:GLU:OE2	13:M:106:LYS:CD	1.87	1.21
17:Q:417:PHE:CE2	18:R:270:PHE:CD1	2.28	1.21
7:G:144:HIS:CG	15:O:146:SER:OG	1.92	1.21
1:A:1329:ILE:HG21	1:A:1456:PHE:CE2	1.75	1.20
3:C:253:PRO:O	14:N:179:ASP:O	1.58	1.20
6:F:72:LYS:HD2	6:F:142:SER:CB	1.69	1.20
1:A:991:LYS:CB	1:A:993:GLN:HB2	1.71	1.20
1:A:824:THR:HB	2:B:1023:ARG:HB2	1.22	1.20
1:A:1003:ARG:NH2	2:B:530:PRO:O	1.74	1.20
1:A:1326:GLU:OE2	1:A:1454:HIS:CB	1.90	1.20
2:B:207:ILE:CD1	2:B:503:VAL:HG21	1.72	1.20
1:A:478:TYR:HA	2:B:1048:SER:O	1.38	1.20
3:C:274:THR:CA	14:N:172:ALA:HB2	1.71	1.20
3:C:296:ASN:O	3:C:298:PHE:CD1	1.94	1.19
1:A:995:TYR:CD2	2:B:708:ASP:CA	2.23	1.19
16:P:436:ILE:CG2	18:R:141:TRP:O	1.91	1.19
18:R:248:LYS:CG	18:R:298:GLN:HE22	1.54	1.19
1:A:1314:GLN:NE2	1:A:1446:ARG:NH1	1.89	1.19
2:B:1072:GLY:N	2:B:1075:GLU:CG	2.04	1.19
2:B:143:TRP:CB	2:B:446:MET:CE	2.13	1.19
2:B:943:ILE:HD12	10:J:44:TYR:CZ	1.78	1.19
1:A:474:LYS:NZ	2:B:1092:LEU:HD23	1.55	1.19
1:A:878:ARG:CG	9:I:67:VAL:HG13	1.73	1.19

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:878:ARG:CD	9:I:66:VAL:CG2	2.21	1.19
2:B:1120:ILE:HD12	15:O:117:GLN:NE2	1.58	1.18
15:O:200:ASN:HB2	17:Q:14:ASN:CA	1.73	1.18
3:C:58:ASN:CA	3:C:296:ASN:ND2	2.06	1.18
15:O:374:PRO:C	15:O:376:TYR:HB3	1.64	1.18
16:P:475:ARG:CB	18:R:1:MET:CE	2.15	1.18
1:A:1313:LEU:HG	1:A:1462:PHE:CE1	1.79	1.18
16:P:399:TRP:CH2	18:R:291:ARG:O	1.95	1.18
1:A:547:ILE:CD1	17:Q:26:ARG:NH2	2.07	1.18
2:B:683:ASN:N	14:N:154:ARG:HH22	1.37	1.18
7:G:24:VAL:O	7:G:128:GLN:CB	1.91	1.18
1:A:474:LYS:CE	2:B:1092:LEU:HD23	1.73	1.17
1:A:1326:GLU:OE1	1:A:1454:HIS:HA	1.45	1.17
7:G:241:ARG:HH11	15:O:189:PHE:CB	1.55	1.17
17:Q:417:PHE:CE2	18:R:270:PHE:HD1	1.60	1.17
18:R:5:PRO:CG	18:R:217:THR:HG21	1.66	1.17
1:A:1050:TYR:CZ	1:A:1179:ILE:HG12	1.79	1.17
16:P:382:GLU:OE1	18:R:146:SER:CB	1.93	1.17
2:B:143:TRP:CD2	2:B:446:MET:CG	2.26	1.17
2:B:679:GLN:HG3	14:N:156:PRO:CA	1.75	1.17
6:F:72:LYS:CA	6:F:142:SER:HB2	1.75	1.17
18:R:6:ILE:HD11	18:R:213:ILE:CB	1.74	1.17
1:A:1322:ILE:HB	1:A:1454:HIS:CE1	1.79	1.17
2:B:152:LEU:HD22	2:B:443:LYS:HD2	1.24	1.17
2:B:894:LYS:HD3	12:L:47:ARG:CZ	1.74	1.17
18:R:199:LYS:HE3	18:R:203:SER:O	1.41	1.17
1:A:477:ASN:O	2:B:1047:ARG:HD3	1.44	1.17
1:A:436:ALA:O	1:A:440:SER:N	1.77	1.16
18:R:4:VAL:HG21	18:R:214:VAL:HG22	1.23	1.16
18:R:251:TRP:CZ3	18:R:307:LYS:HE2	1.80	1.16
16:P:438:TRP:CD1	18:R:141:TRP:CZ2	2.33	1.16
1:A:438:ILE:O	1:A:457:LYS:CD	1.94	1.16
1:A:953:GLU:HA	1:A:1205:PHE:CD2	1.81	1.16
2:B:1072:GLY:N	2:B:1075:GLU:HG3	1.59	1.16
1:A:995:TYR:HD2	2:B:708:ASP:CA	1.59	1.15
1:A:1657:LEU:O	6:F:133:VAL:N	1.76	1.15
1:A:1657:LEU:HD22	7:G:104:LEU:CD1	1.74	1.15
2:B:19:LEU:HD13	10:J:26:GLN:OE1	1.30	1.15
7:G:141:SER:HB2	15:O:142:ILE:HD12	1.20	1.15
2:B:266:LYS:HG3	2:B:473:GLN:O	1.46	1.15
16:P:185:GLN:HA	18:R:196:GLU:O	1.42	1.15

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:P:436:ILE:HG23	18:R:141:TRP:O	0.97	1.15
1:A:435:ASN:O	1:A:439:ASP:O	1.61	1.15
16:P:390:GLN:HB2	18:R:150:GLN:O	1.37	1.15
2:B:149:GLU:OE1	2:B:441:LYS:NZ	1.80	1.15
2:B:894:LYS:CG	12:L:54:ARG:HH22	1.53	1.15
1:A:566:SER:CB	15:O:235:GLU:CD	2.15	1.15
1:A:990:ILE:HD11	1:A:995:TYR:HA	1.24	1.15
3:C:274:THR:HA	14:N:172:ALA:CB	1.75	1.15
1:A:1482:LYS:HE2	2:B:304:ASP:OD1	0.96	1.14
2:B:266:LYS:HE3	2:B:473:GLN:O	1.46	1.14
1:A:952:LEU:HD22	1:A:1004:GLU:HG3	1.15	1.14
2:B:566:TYR:HD2	13:M:73:SER:OG	1.23	1.14
2:B:894:LYS:HD3	12:L:47:ARG:NE	1.63	1.14
17:Q:22:ILE:CD1	17:Q:24:ASP:OD2	1.96	1.14
1:A:1329:ILE:CG2	1:A:1456:PHE:CE2	2.31	1.14
1:A:1657:LEU:HD22	7:G:104:LEU:HD13	1.14	1.14
2:B:985:ILE:O	14:N:160:VAL:HG23	1.46	1.14
14:N:87:TYR:CZ	14:N:141:GLU:OE1	2.01	1.14
1:A:991:LYS:H	1:A:994:GLU:CG	1.60	1.14
3:C:253:PRO:CD	14:N:180:PHE:CB	1.85	1.14
17:Q:417:PHE:CZ	18:R:270:PHE:HD1	1.65	1.14
1:A:438:ILE:O	1:A:457:LYS:HD2	1.42	1.14
1:A:436:ALA:HB2	1:A:443:ALA:HB2	1.15	1.13
2:B:1089:GLN:CG	2:B:1093:LEU:CD2	2.24	1.13
15:O:240:ILE:CG2	15:O:380:SER:HB3	1.77	1.13
17:Q:134:LYS:O	17:Q:138:LEU:HB2	1.47	1.13
18:R:203:SER:HA	20:R:601:SO4:O3	1.38	1.13
1:A:403:LEU:CD1	1:A:419:ILE:HG21	1.78	1.13
2:B:1072:GLY:H	2:B:1075:GLU:HG3	1.08	1.13
2:B:1093:LEU:HG	2:B:1094:ASN:OD1	1.45	1.13
15:O:248:LEU:HD11	15:O:598:PHE:HD2	1.05	1.13
16:P:475:ARG:CB	18:R:1:MET:HE1	1.73	1.13
17:Q:9:ILE:HG13	17:Q:10:CYS:H	1.06	1.13
18:R:5:PRO:CD	18:R:217:THR:OG1	1.95	1.13
1:A:474:LYS:NZ	2:B:1092:LEU:CD2	2.11	1.12
1:A:1276:THR:N	9:I:45:LEU:O	1.80	1.12
2:B:1072:GLY:H	2:B:1075:GLU:CG	1.59	1.12
1:A:756:LYS:CD	9:I:85:LYS:HZ1	1.49	1.12
1:A:1556:GLU:OE2	5:E:212:ARG:NH1	1.82	1.12
18:R:248:LYS:HG2	18:R:298:GLN:NE2	1.62	1.12
1:A:435:ASN:O	1:A:439:ASP:HB3	1.50	1.12

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:894:LYS:CG	12:L:54:ARG:NH2	1.92	1.12
1:A:990:ILE:CA	1:A:994:GLU:HB2	1.78	1.12
7:G:241:ARG:HH11	15:O:189:PHE:HB2	1.10	1.12
16:P:348:HIS:CD2	18:R:154:LYS:HD3	1.82	1.12
1:A:566:SER:CB	15:O:235:GLU:OE2	1.96	1.12
3:C:334:THR:HG21	11:K:44:ARG:HB3	1.29	1.12
7:G:143:SER:O	15:O:105:ASN:ND2	1.82	1.12
1:A:472:MET:HB3	2:B:1073:GLU:CB	1.80	1.11
3:C:230:LEU:HD12	3:C:231:PRO:HD2	1.22	1.11
18:R:248:LYS:CG	18:R:298:GLN:NE2	2.12	1.11
2:B:1002:LYS:CD	14:N:166:LEU:O	1.99	1.11
1:A:429:THR:CG2	18:R:406:LYS:HE3	1.81	1.11
1:A:878:ARG:CB	9:I:67:VAL:CG1	2.27	1.11
15:O:376:TYR:CZ	15:O:377:TYR:CE2	2.37	1.11
2:B:145:VAL:HG11	2:B:441:LYS:HG2	1.24	1.11
1:A:475:ARG:CZ	2:B:1061:LYS:HB2	1.81	1.11
2:B:1003:ALA:HA	14:N:169:GLU:H	1.04	1.11
17:Q:358:PRO:CA	18:R:206:ARG:NH1	2.11	1.10
1:A:503:VAL:HG23	1:A:530:TRP:HB2	1.29	1.10
1:A:1049:MET:CG	1:A:1052:GLY:C	2.18	1.10
1:A:1482:LYS:O	2:B:308:LEU:HD21	1.50	1.10
1:A:474:LYS:HE3	2:B:1092:LEU:CD2	1.80	1.10
1:A:474:LYS:O	2:B:1070:ARG:CB	2.00	1.10
1:A:545:SER:H	17:Q:34:VAL:HG23	1.08	1.10
1:A:1299:ASN:OD1	1:A:1467:GLY:HA3	1.39	1.10
6:F:75:PRO:HG2	6:F:78:GLN:HB2	1.13	1.10
15:O:373:LEU:O	15:O:376:TYR:HB2	1.51	1.10
2:B:551:ILE:HG21	2:B:647:SER:HA	1.29	1.09
2:B:985:ILE:HB	14:N:160:VAL:CG2	1.82	1.09
13:M:61:GLU:OE2	13:M:106:LYS:HD3	1.44	1.09
15:O:517:LEU:HA	15:O:525:MET:HE2	1.34	1.09
17:Q:188:ALA:HB3	17:Q:384:GLN:CG	1.82	1.09
17:Q:356:VAL:HG11	18:R:208:TYR:CE1	1.85	1.09
15:O:579:LEU:HA	15:O:582:ARG:HB3	1.24	1.09
18:R:4:VAL:CG2	18:R:214:VAL:HG22	1.83	1.09
1:A:1600:ARG:NH2	1:A:1617:THR:OG1	1.83	1.09
16:P:397:LYS:NZ	18:R:85:ARG:HD3	1.62	1.09
17:Q:26:ARG:HB3	17:Q:34:VAL:HG13	1.12	1.09
1:A:1314:GLN:HE21	1:A:1446:ARG:NH1	1.46	1.09
6:F:72:LYS:HA	6:F:142:SER:HB2	1.21	1.09
6:F:74:ILE:CG1	6:F:75:PRO:HD2	1.83	1.09

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:O:234:ILE:HG22	15:O:237:ILE:HG12	1.25	1.09
15:O:374:PRO:O	15:O:376:TYR:HB3	1.53	1.09
17:Q:417:PHE:HE2	18:R:270:PHE:CD1	1.69	1.09
1:A:990:ILE:HB	1:A:994:GLU:HB3	1.17	1.08
1:A:1322:ILE:CD1	1:A:1457:ILE:HD11	1.83	1.08
1:A:1575:ILE:N	9:I:122:ARG:NH1	2.00	1.08
3:C:272:LYS:HG2	14:N:175:TYR:CD1	1.88	1.08
18:R:5:PRO:CD	18:R:217:THR:CB	2.31	1.08
1:A:1049:MET:HG2	1:A:1053:ASP:N	1.66	1.08
2:B:527:PHE:CE1	2:B:666:PRO:CG	2.35	1.08
2:B:849:GLY:CA	12:L:60:ARG:HH22	1.57	1.08
17:Q:20:TRP:CZ3	17:Q:22:ILE:HG22	1.58	1.08
7:G:159:LYS:HD2	15:O:103:ASN:CG	1.72	1.08
1:A:476:VAL:HG22	2:B:1070:ARG:H	1.15	1.08
15:O:376:TYR:CE2	15:O:377:TYR:HE2	1.66	1.08
16:P:184:SER:HB3	18:R:198:LEU:CB	1.75	1.08
1:A:878:ARG:HB3	9:I:67:VAL:HG11	1.16	1.08
16:P:622:TYR:O	16:P:626:LEU:HB2	1.54	1.08
1:A:486:PRO:O	2:B:781:TYR:CD2	2.06	1.07
1:A:597:LYS:CB	2:B:1082:HIS:NE2	2.17	1.07
1:A:999:CYS:HA	2:B:712:SER:HB2	1.32	1.07
3:C:253:PRO:N	14:N:180:PHE:CD1	2.19	1.07
15:O:200:ASN:ND2	17:Q:14:ASN:O	1.86	1.07
1:A:474:LYS:HZ2	2:B:1092:LEU:HA	1.11	1.07
1:A:506:THR:HG22	1:A:579:ARG:C	1.74	1.07
1:A:1322:ILE:HB	1:A:1454:HIS:NE2	1.68	1.07
2:B:943:ILE:HD12	10:J:44:TYR:CE1	1.88	1.07
6:F:72:LYS:CD	6:F:142:SER:CB	2.28	1.07
7:G:141:SER:HB3	15:O:142:ILE:HD13	1.35	1.07
1:A:954:GLY:HA3	1:A:1205:PHE:HB3	1.27	1.07
1:A:1314:GLN:NE2	1:A:1446:ARG:HD2	1.67	1.07
1:A:474:LYS:CE	2:B:1092:LEU:CD2	2.32	1.07
1:A:834:ARG:NH2	2:B:994:ASP:OD1	1.87	1.07
1:A:506:THR:HG22	1:A:579:ARG:O	1.53	1.07
1:A:1049:MET:HB3	1:A:1052:GLY:CA	1.84	1.07
7:G:159:LYS:CD	15:O:103:ASN:OD1	2.02	1.07
1:A:564:PRO:HG2	15:O:370:THR:O	1.53	1.06
1:A:1326:GLU:OE2	1:A:1454:HIS:C	1.93	1.06
2:B:1089:GLN:HG3	2:B:1093:LEU:CB	1.82	1.06
18:R:251:TRP:CE3	18:R:307:LYS:HE2	1.86	1.06
1:A:878:ARG:HG2	9:I:67:VAL:HG13	1.09	1.06

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1322:ILE:HG21	1:A:1454:HIS:CG	1.81	1.06
16:P:436:ILE:HB	18:R:143:THR:HG23	1.30	1.06
1:A:88:PRO:CG	1:A:438:ILE:HD12	1.83	1.06
3:C:58:ASN:CA	3:C:296:ASN:HD21	1.65	1.06
6:F:74:ILE:O	7:G:95:LEU:HD11	1.43	1.06
17:Q:351:ASN:HB3	17:Q:369:TRP:CZ3	1.89	1.06
1:A:1317:ILE:CG2	1:A:1460:TYR:HE1	1.69	1.06
1:A:1575:ILE:HG13	9:I:122:ARG:NH1	0.74	1.06
2:B:49:PHE:HB2	2:B:164:MET:CE	1.84	1.06
1:A:597:LYS:CB	2:B:1082:HIS:CD2	2.38	1.06
2:B:849:GLY:C	12:L:60:ARG:HH22	1.58	1.06
1:A:1326:GLU:OE1	1:A:1454:HIS:CA	2.03	1.05
2:B:1092:LEU:HA	2:B:1096:SER:HB2	1.35	1.05
1:A:1050:TYR:CE1	1:A:1179:ILE:HG12	1.90	1.05
1:A:1313:LEU:HG	1:A:1462:PHE:CZ	1.90	1.05
1:A:1660:VAL:O	7:G:102:GLU:HG2	1.54	1.05
2:B:143:TRP:CD2	2:B:446:MET:SD	2.49	1.05
16:P:197:ARG:NE	16:P:261:VAL:H	1.54	1.05
2:B:207:ILE:CD1	2:B:503:VAL:CG2	2.34	1.05
17:Q:17:SER:O	17:Q:29:CYS:HB2	1.55	1.05
1:A:422:ARG:NH1	18:R:412:ARG:NH1	2.04	1.05
1:A:566:SER:HB3	15:O:235:GLU:OE2	1.56	1.05
1:A:1600:ARG:CD	1:A:1616:GLU:OE1	2.05	1.05
2:B:527:PHE:CE2	2:B:666:PRO:HA	1.89	1.05
15:O:240:ILE:HG22	15:O:380:SER:HB3	1.06	1.05
16:P:389:TRP:HH2	18:R:148:ASN:N	1.54	1.05
18:R:6:ILE:CD1	18:R:213:ILE:HB	1.87	1.05
1:A:545:SER:N	17:Q:34:VAL:CG2	2.18	1.05
16:P:434:ARG:HG2	18:R:143:THR:CG2	1.87	1.05
1:A:503:VAL:CA	1:A:580:HIS:CD2	2.23	1.04
1:A:1298:ASP:OD1	1:A:1468:LYS:NZ	1.90	1.04
2:B:49:PHE:HB2	2:B:164:MET:HE1	1.06	1.04
16:P:434:ARG:HG2	18:R:143:THR:HG21	1.38	1.04
17:Q:356:VAL:HG13	18:R:212:HIS:CE1	1.91	1.04
16:P:22:GLY:CA	18:R:139:GLU:OE2	2.04	1.04
1:A:1322:ILE:CB	1:A:1454:HIS:CE1	2.40	1.04
2:B:889:GLY:HA3	12:L:54:ARG:O	1.56	1.04
16:P:475:ARG:HB3	18:R:1:MET:CE	1.85	1.04
17:Q:15:CYS:HB3	17:Q:17:SER:N	1.70	1.04
18:R:4:VAL:HG21	18:R:214:VAL:CG2	1.88	1.04
1:A:615:ARG:NH1	2:B:929:ARG:HE	1.54	1.04

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:878:ARG:CD	9:I:66:VAL:HG23	1.68	1.04
1:A:1049:MET:CB	1:A:1052:GLY:HA2	1.88	1.04
16:P:475:ARG:HB3	18:R:1:MET:HE1	1.08	1.04
1:A:477:ASN:O	2:B:1047:ARG:CD	2.06	1.04
1:A:566:SER:HB2	15:O:235:GLU:CD	1.77	1.04
2:B:551:ILE:HG23	2:B:648:ARG:N	1.73	1.04
15:O:234:ILE:HG23	15:O:237:ILE:HG12	1.37	1.04
16:P:436:ILE:HG22	18:R:143:THR:N	1.72	1.04
16:P:472:ARG:CZ	18:R:200:THR:HG23	1.87	1.04
18:R:5:PRO:HD3	18:R:217:THR:OG1	1.55	1.04
1:A:1003:ARG:HH21	2:B:530:PRO:C	1.61	1.03
1:A:1657:LEU:CD2	7:G:104:LEU:HD13	1.88	1.03
15:O:243:GLU:OE1	15:O:328:LEU:HD23	1.58	1.03
17:Q:413:LEU:HG	18:R:273:TRP:HZ2	1.16	1.03
1:A:1049:MET:CG	1:A:1053:ASP:N	2.21	1.03
1:A:1322:ILE:CG2	1:A:1454:HIS:CE1	2.41	1.03
1:A:1326:GLU:CD	1:A:1454:HIS:CB	2.26	1.03
2:B:1089:GLN:HG2	2:B:1093:LEU:HD22	1.07	1.03
6:F:72:LYS:HB3	6:F:142:SER:CB	1.87	1.03
7:G:143:SER:HB3	15:O:104:ILE:H	0.90	1.03
17:Q:417:PHE:CZ	18:R:270:PHE:CD1	2.45	1.03
18:R:314:TRP:NE1	18:R:363:GLU:OE2	1.92	1.03
1:A:476:VAL:O	2:B:1068:GLY:HA3	1.57	1.03
2:B:182:GLN:HE22	10:J:69:ARG:HB3	1.23	1.03
3:C:296:ASN:O	3:C:298:PHE:CE1	2.10	1.03
16:P:486:ALA:O	18:R:137:SER:N	1.92	1.03
17:Q:5:ILE:O	17:Q:19:LEU:O	1.74	1.03
1:A:938:VAL:HG22	9:I:82:ILE:CD1	1.88	1.03
2:B:527:PHE:CD1	2:B:666:PRO:CG	2.40	1.03
1:A:503:VAL:CG2	1:A:530:TRP:HB2	1.88	1.03
1:A:721:LYS:O	8:H:96:VAL:N	1.91	1.03
16:P:382:GLU:OE1	18:R:146:SER:HB3	1.56	1.03
1:A:545:SER:HB2	17:Q:34:VAL:HG22	1.41	1.02
1:A:991:LYS:HB2	1:A:993:GLN:HB2	1.35	1.02
2:B:681:ILE:HB	14:N:154:ARG:HG3	1.40	1.02
7:G:144:HIS:CD2	15:O:146:SER:CA	2.42	1.02
18:R:199:LYS:HE2	18:R:204:GLU:HB3	1.22	1.02
1:A:1317:ILE:HG21	1:A:1460:TYR:HE1	1.22	1.02
2:B:682:GLN:CA	14:N:154:ARG:NH2	2.22	1.02
7:G:144:HIS:CD2	15:O:146:SER:HA	1.93	1.02
15:O:379:ARG:HA	15:O:379:ARG:HH11	1.22	1.02

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:Q:188:ALA:CB	17:Q:384:GLN:CG	2.36	1.02
1:A:566:SER:HB3	15:O:235:GLU:CD	1.77	1.02
1:A:878:ARG:HG2	9:I:66:VAL:HG23	1.38	1.02
2:B:566:TYR:CD2	13:M:73:SER:OG	2.11	1.02
2:B:1089:GLN:HG3	2:B:1093:LEU:CD1	1.87	1.02
7:G:159:LYS:HB2	15:O:105:ASN:HD22	1.24	1.02
1:A:472:MET:CB	2:B:1073:GLU:HB2	1.89	1.02
1:A:878:ARG:CG	9:I:66:VAL:CG2	2.36	1.02
16:P:432:PRO:O	18:R:145:SER:OG	1.78	1.02
1:A:909:SER:HA	9:I:83:LYS:NZ	1.75	1.02
3:C:253:PRO:CD	14:N:180:PHE:CD1	2.43	1.02
16:P:397:LYS:NZ	18:R:85:ARG:NE	2.00	1.02
6:F:72:LYS:CB	6:F:142:SER:CB	2.37	1.01
16:P:473:HIS:CD2	18:R:1:MET:SD	2.53	1.01
17:Q:413:LEU:HG	18:R:273:TRP:CZ2	1.95	1.01
1:A:1003:ARG:NH2	2:B:530:PRO:C	2.14	1.01
2:B:143:TRP:CE2	2:B:446:MET:HB2	1.96	1.01
3:C:229:LEU:HD22	3:C:295:ARG:O	1.61	1.01
16:P:22:GLY:N	18:R:139:GLU:OE2	1.93	1.01
18:R:6:ILE:HD11	18:R:213:ILE:HB	1.37	1.01
1:A:995:TYR:OH	2:B:707:SER:HB2	0.83	1.01
3:C:228:ARG:NH1	14:N:173:THR:O	1.90	1.01
18:R:199:LYS:CE	18:R:204:GLU:CA	2.37	1.01
2:B:143:TRP:CB	2:B:446:MET:SD	2.48	1.01
18:R:5:PRO:HG2	18:R:217:THR:CB	1.75	1.01
1:A:486:PRO:HD2	2:B:928:SER:OG	1.60	1.01
2:B:1071:VAL:HG21	2:B:1091:ARG:HG3	1.41	1.01
15:O:332:LEU:HD11	15:O:380:SER:OG	1.61	1.01
1:A:954:GLY:CA	1:A:1205:PHE:HB3	1.89	1.00
1:A:990:ILE:CG1	1:A:995:TYR:N	2.24	1.00
2:B:894:LYS:HG3	12:L:54:ARG:NH2	1.41	1.00
2:B:1089:GLN:HG3	2:B:1093:LEU:HB2	1.42	1.00
3:C:293:ARG:H	3:C:295:ARG:CZ	1.74	1.00
17:Q:12:THR:CB	17:Q:33:HIS:CE1	2.44	1.00
1:A:88:PRO:HG2	1:A:438:ILE:CD1	1.91	1.00
16:P:274:ILE:O	16:P:289:SER:HB2	1.57	1.00
1:A:1314:GLN:NE2	1:A:1446:ARG:HH11	1.48	1.00
2:B:75:ASP:HB3	2:B:440:PHE:CZ	1.96	1.00
3:C:253:PRO:HD2	14:N:180:PHE:CD1	1.95	1.00
16:P:399:TRP:HH2	18:R:291:ARG:O	1.35	1.00
17:Q:9:ILE:HB	17:Q:16:PRO:HB2	1.43	1.00

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:Q:188:ALA:HB3	17:Q:384:GLN:HG2	1.43	1.00
18:R:177:LEU:O	18:R:185:LYS:CE	2.08	1.00
1:A:1322:ILE:HD12	1:A:1457:ILE:HD11	1.04	1.00
7:G:24:VAL:HA	7:G:25:THR:HA	1.44	1.00
15:O:240:ILE:O	15:O:380:SER:OG	1.80	1.00
2:B:19:LEU:HD11	10:J:26:GLN:OE1	1.61	1.00
7:G:159:LYS:CB	15:O:105:ASN:ND2	2.23	1.00
16:P:185:GLN:HG3	18:R:190:SER:HB3	1.42	1.00
1:A:995:TYR:CE2	2:B:708:ASP:HA	1.97	1.00
1:A:1310:LYS:HG2	1:A:1311:GLU:CD	1.77	1.00
2:B:143:TRP:CZ3	2:B:446:MET:HG3	1.96	1.00
2:B:1072:GLY:O	2:B:1075:GLU:CG	2.09	1.00
18:R:5:PRO:HG2	18:R:217:THR:HG22	1.44	1.00
2:B:1092:LEU:O	2:B:1096:SER:HB3	1.59	0.99
7:G:143:SER:CB	15:O:104:ILE:H	1.74	0.99
13:M:102:SER:O	13:M:105:SER:N	1.95	0.99
17:Q:351:ASN:CA	17:Q:369:TRP:CH2	2.45	0.99
1:A:1297:PHE:CE2	1:A:1301:GLU:CD	2.34	0.99
1:A:995:TYR:CZ	2:B:715:ASN:ND2	2.29	0.99
1:A:998:HIS:NE2	2:B:711:GLN:HG3	1.75	0.99
15:O:202:ASN:HB3	17:Q:31:TYR:OH	1.62	0.99
1:A:408:LYS:CB	1:A:411:VAL:HB	1.92	0.99
1:A:425:ASN:CG	18:R:406:LYS:HZ2	1.64	0.99
1:A:629:ASP:C	2:B:926:VAL:CG2	2.31	0.99
1:A:1050:TYR:CG	1:A:1179:ILE:HG21	1.96	0.99
6:F:74:ILE:HG12	6:F:75:PRO:CD	1.91	0.99
15:O:348:THR:HG22	15:O:351:SER:HB3	1.42	0.99
17:Q:22:ILE:CD1	17:Q:26:ARG:NE	2.25	0.99
16:P:389:TRP:CH2	18:R:148:ASN:N	2.29	0.99
1:A:435:ASN:HB3	1:A:442:LYS:HB3	1.43	0.99
15:O:376:TYR:CE1	15:O:588:LEU:CD2	2.45	0.99
16:P:184:SER:HB3	18:R:198:LEU:H	1.25	0.99
14:N:86:ASP:O	14:N:142:THR:N	1.94	0.99
16:P:397:LYS:CE	18:R:85:ARG:CD	2.40	0.99
1:A:435:ASN:HB3	1:A:442:LYS:HB2	1.40	0.99
1:A:1314:GLN:HE22	1:A:1446:ARG:HD2	1.28	0.99
18:R:6:ILE:HD11	18:R:213:ILE:HG22	1.42	0.99
1:A:478:TYR:CA	2:B:1048:SER:O	2.10	0.99
16:P:397:LYS:HZ1	18:R:85:ARG:NE	1.58	0.99
1:A:1330:VAL:CG2	1:A:1455:ARG:CZ	2.41	0.98
2:B:143:TRP:CE3	2:B:446:MET:CG	2.46	0.98

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:144:HIS:NE2	15:O:145:SER:HB3	1.78	0.98
18:R:199:LYS:CE	18:R:204:GLU:CB	2.32	0.98
2:B:824:HIS:ND1	2:B:897:GLU:OE1	1.90	0.98
7:G:143:SER:HB3	15:O:104:ILE:N	1.75	0.98
1:A:566:SER:HB2	15:O:235:GLU:OE1	1.61	0.98
17:Q:9:ILE:HG13	17:Q:10:CYS:N	1.77	0.98
1:A:684:ASP:CG	8:H:20:TYR:HB3	1.83	0.98
2:B:1072:GLY:CA	2:B:1075:GLU:HG2	1.93	0.98
1:A:1276:THR:CB	9:I:45:LEU:HD12	1.93	0.98
2:B:697:LEU:HB2	2:B:702:ASN:ND2	1.77	0.98
3:C:41:GLU:OE2	11:K:138:LYS:HE3	1.64	0.98
3:C:272:LYS:CA	14:N:175:TYR:CZ	2.16	0.98
1:A:480:ALA:CB	2:B:1046:VAL:HG23	1.93	0.98
1:A:436:ALA:C	1:A:439:ASP:C	2.22	0.98
1:A:990:ILE:CB	1:A:994:GLU:CB	1.98	0.98
1:A:1317:ILE:CG2	1:A:1460:TYR:CE1	2.45	0.98
1:A:438:ILE:O	1:A:457:LYS:CB	2.12	0.98
1:A:721:LYS:NZ	8:H:90:ALA:O	1.97	0.98
1:A:1314:GLN:NE2	1:A:1446:ARG:CD	2.25	0.98
16:P:397:LYS:HZ3	18:R:85:ARG:HD3	1.13	0.98
1:A:422:ARG:HH12	18:R:412:ARG:CZ	1.77	0.98
1:A:995:TYR:CZ	2:B:707:SER:HB2	1.98	0.97
2:B:71:LYS:HD3	2:B:421:LEU:HD13	1.46	0.97
2:B:1003:ALA:HA	14:N:169:GLU:N	1.78	0.97
1:A:1276:THR:HG1	9:I:45:LEU:HD12	1.18	0.97
13:M:102:SER:O	13:M:105:SER:CA	2.11	0.97
1:A:472:MET:HB3	2:B:1073:GLU:HB2	0.99	0.97
1:A:991:LYS:H	1:A:994:GLU:HG3	0.82	0.97
1:A:953:GLU:CA	1:A:1205:PHE:CD2	2.46	0.97
2:B:943:ILE:CD1	10:J:44:TYR:CE1	2.46	0.97
16:P:184:SER:CA	18:R:198:LEU:HB3	1.94	0.97
1:A:909:SER:HA	9:I:83:LYS:CE	1.93	0.97
2:B:152:LEU:HD22	2:B:443:LYS:CD	1.94	0.97
2:B:207:ILE:HD11	2:B:503:VAL:HG21	1.43	0.97
1:A:535:GLN:HE22	17:Q:26:ARG:CD	1.77	0.97
18:R:248:LYS:HG3	18:R:298:GLN:HE22	1.26	0.97
1:A:1314:GLN:CD	1:A:1446:ARG:HD2	1.84	0.97
2:B:550:ARG:HB2	2:B:650:LEU:HB2	1.47	0.97
17:Q:15:CYS:SG	17:Q:17:SER:HB2	2.05	0.97
1:A:545:SER:H	17:Q:34:VAL:CG2	1.74	0.97
1:A:615:ARG:HH22	2:B:929:ARG:HG2	1.27	0.97

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:999:CYS:CA	2:B:712:SER:CB	2.43	0.97
1:A:1050:TYR:CD1	1:A:1179:ILE:HG21	1.99	0.97
2:B:207:ILE:HG13	2:B:503:VAL:HG22	1.47	0.97
2:B:75:ASP:CB	2:B:440:PHE:CE2	2.47	0.96
15:O:376:TYR:HE1	15:O:588:LEU:CD2	1.77	0.96
16:P:185:GLN:HB3	18:R:195:LEU:HB3	1.47	0.96
1:A:88:PRO:HG2	1:A:438:ILE:HD12	0.97	0.96
2:B:202:LEU:HD22	2:B:488:ALA:HB2	1.46	0.96
1:A:1049:MET:HB3	1:A:1052:GLY:N	1.79	0.96
13:M:102:SER:OG	13:M:105:SER:N	1.96	0.96
18:R:15:GLN:CD	18:R:184:ASN:HD22	1.69	0.96
1:A:474:LYS:NZ	2:B:1092:LEU:HA	1.80	0.96
2:B:1089:GLN:HG3	2:B:1093:LEU:CD2	1.90	0.96
6:F:66:ARG:NH2	7:G:90:LEU:CD1	2.29	0.96
17:Q:193:PHE:CD2	18:R:208:TYR:CD2	2.53	0.96
2:B:68:ILE:HG23	2:B:71:LYS:HZ2	1.23	0.96
16:P:436:ILE:HB	18:R:143:THR:CG2	1.95	0.96
1:A:474:LYS:O	2:B:1070:ARG:CA	2.14	0.96
1:A:474:LYS:O	2:B:1070:ARG:HA	1.65	0.96
1:A:991:LYS:HB3	1:A:993:GLN:CD	1.84	0.96
2:B:796:ARG:CZ	10:J:8:PHE:O	2.14	0.96
1:A:953:GLU:HG2	1:A:1205:PHE:CE2	1.99	0.96
15:O:243:GLU:HB3	15:O:332:LEU:HD13	1.48	0.96
1:A:990:ILE:CD1	1:A:995:TYR:HA	1.96	0.96
17:Q:371:GLU:HG3	18:R:231:LEU:CD1	1.96	0.96
2:B:49:PHE:CB	2:B:164:MET:HE1	1.96	0.95
18:R:6:ILE:CD1	18:R:213:ILE:CG2	2.43	0.95
2:B:68:ILE:CG2	2:B:71:LYS:HZ2	1.65	0.95
16:P:349:GLY:HA2	18:R:153:ASN:O	1.64	0.95
17:Q:22:ILE:HD11	17:Q:26:ARG:NE	1.81	0.95
18:R:199:LYS:HE2	18:R:204:GLU:N	1.82	0.95
1:A:429:THR:CG2	18:R:406:LYS:CE	2.42	0.95
1:A:862:THR:CB	9:I:67:VAL:HG12	1.95	0.95
1:A:1484:LEU:HD13	2:B:305:ARG:NH1	1.80	0.95
17:Q:410:ARG:NH2	18:R:278:TYR:OH	1.99	0.95
1:A:1322:ILE:CD1	1:A:1457:ILE:CD1	2.43	0.95
2:B:152:LEU:CA	2:B:443:LYS:HE3	1.96	0.95
2:B:209:GLN:HG2	2:B:210:ARG:H	1.32	0.95
15:O:376:TYR:OH	15:O:588:LEU:HD21	1.65	0.95
18:R:199:LYS:CE	18:R:203:SER:O	2.13	0.95
1:A:545:SER:CA	17:Q:34:VAL:CG2	2.36	0.95

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:547:ILE:CD1	17:Q:26:ARG:HH22	1.71	0.95
1:A:1484:LEU:HD13	2:B:305:ARG:NE	1.81	0.95
6:F:75:PRO:CG	6:F:78:GLN:HB2	1.96	0.95
1:A:1322:ILE:CB	1:A:1454:HIS:NE2	2.30	0.95
1:A:474:LYS:O	2:B:1070:ARG:HB2	1.66	0.95
1:A:953:GLU:C	1:A:1205:PHE:CG	2.40	0.95
15:O:247:GLU:OE1	15:O:325:ILE:HG12	1.10	0.95
1:A:429:THR:HG23	18:R:406:LYS:HZ1	1.31	0.95
2:B:1089:GLN:CG	2:B:1093:LEU:HD13	1.96	0.95
13:M:102:SER:CB	13:M:105:SER:CB	2.02	0.95
17:Q:341:ARG:NH1	17:Q:369:TRP:HE1	1.65	0.95
2:B:1093:LEU:O	2:B:1098:TYR:HB2	1.67	0.94
16:P:443:ASP:O	18:R:3:GLU:CB	2.15	0.94
2:B:207:ILE:HG13	2:B:503:VAL:HG23	1.48	0.94
6:F:74:ILE:HG12	6:F:75:PRO:HD2	0.95	0.94
1:A:545:SER:N	17:Q:34:VAL:HG23	1.77	0.94
17:Q:9:ILE:CG1	17:Q:10:CYS:H	1.79	0.94
1:A:588:LEU:HD21	2:B:1087:LEU:HD13	1.48	0.94
1:A:1049:MET:CB	1:A:1052:GLY:CA	2.44	0.94
16:P:433:VAL:CA	18:R:145:SER:OG	2.13	0.94
16:P:436:ILE:HG21	18:R:142:ARG:O	1.67	0.94
1:A:506:THR:HA	1:A:579:ARG:O	1.67	0.94
1:A:543:LEU:HB2	17:Q:34:VAL:O	1.67	0.94
1:A:672:ASP:OD2	2:B:777:SER:HB3	1.67	0.94
1:A:991:LYS:HB3	1:A:993:GLN:OE1	1.64	0.94
2:B:679:GLN:HG3	14:N:155:VAL:O	1.64	0.94
2:B:75:ASP:N	2:B:440:PHE:HE2	1.65	0.94
2:B:1003:ALA:CA	14:N:169:GLU:H	1.80	0.94
17:Q:358:PRO:HA	18:R:206:ARG:HH12	0.78	0.94
15:O:63:LEU:HD12	15:O:71:ILE:HG13	1.47	0.94
16:P:184:SER:HB3	18:R:198:LEU:N	1.81	0.94
16:P:390:GLN:HB3	18:R:150:GLN:O	1.68	0.94
18:R:251:TRP:HE3	18:R:307:LYS:CE	1.69	0.94
1:A:1600:ARG:HD2	1:A:1616:GLU:OE1	1.67	0.94
2:B:1089:GLN:HG3	2:B:1093:LEU:HD13	1.49	0.94
15:O:376:TYR:CZ	15:O:588:LEU:HD21	2.03	0.94
1:A:506:THR:CB	1:A:579:ARG:O	2.16	0.94
17:Q:341:ARG:NH1	17:Q:369:TRP:NE1	2.16	0.94
1:A:1482:LYS:HE2	2:B:304:ASP:CG	1.87	0.93
1:A:506:THR:CG2	1:A:579:ARG:O	2.15	0.93
1:A:938:VAL:HG22	9:I:82:ILE:HD13	1.49	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:145:VAL:HG21	2:B:441:LYS:HA	1.47	0.93
17:Q:22:ILE:HD12	17:Q:24:ASP:OD2	1.68	0.93
1:A:1484:LEU:HD13	2:B:305:ARG:NH2	1.82	0.93
2:B:182:GLN:NE2	10:J:69:ARG:CB	2.32	0.93
18:R:199:LYS:CE	20:R:601:SO4:O2	2.17	0.93
1:A:991:LYS:HB3	1:A:993:GLN:HB2	1.50	0.93
2:B:202:LEU:HD23	2:B:202:LEU:H	1.34	0.93
15:O:376:TYR:CD1	15:O:419:LYS:HE2	2.02	0.93
1:A:613:THR:HG21	2:B:913:ILE:CG2	1.98	0.93
2:B:1072:GLY:N	2:B:1075:GLU:HG2	1.80	0.93
16:P:405:TYR:HE1	16:P:414:ILE:HG23	1.31	0.93
15:O:233:LEU:O	15:O:237:ILE:HD12	1.65	0.93
18:R:5:PRO:HG3	18:R:217:THR:CB	1.71	0.93
1:A:756:LYS:CD	9:I:85:LYS:HZ3	1.76	0.92
16:P:24:SER:HB2	18:R:318:ILE:HD11	1.50	0.92
1:A:1049:MET:HB3	1:A:1052:GLY:HA2	1.42	0.92
2:B:205:MET:HE1	2:B:500:PHE:O	1.68	0.92
2:B:1002:LYS:HD2	14:N:166:LEU:HB2	1.51	0.92
16:P:399:TRP:CZ3	18:R:291:ARG:O	2.22	0.92
17:Q:188:ALA:HB3	17:Q:384:GLN:CB	1.98	0.92
2:B:849:GLY:CA	12:L:60:ARG:NH2	2.17	0.92
2:B:1089:GLN:HG2	2:B:1093:LEU:CD2	1.90	0.92
17:Q:26:ARG:CB	17:Q:34:VAL:HG13	1.99	0.92
1:A:436:ALA:HA	1:A:439:ASP:O	1.68	0.92
1:A:720:PHE:CE2	8:H:141:TYR:HE2	1.86	0.92
2:B:890:ASP:O	12:L:54:ARG:CD	2.15	0.92
16:P:184:SER:HA	18:R:198:LEU:HB3	1.49	0.92
2:B:549:CYS:SG	2:B:649:MET:CG	2.57	0.92
17:Q:15:CYS:HB3	17:Q:16:PRO:CA	2.00	0.92
17:Q:417:PHE:HE2	18:R:270:PHE:CE1	1.86	0.92
2:B:679:GLN:HG2	14:N:156:PRO:C	1.67	0.92
3:C:272:LYS:HG2	14:N:175:TYR:HD1	1.28	0.92
3:C:294:VAL:O	3:C:297:HIS:HB3	1.70	0.92
1:A:630:GLY:N	2:B:926:VAL:HG21	1.84	0.92
2:B:266:LYS:CG	2:B:473:GLN:O	2.18	0.92
18:R:199:LYS:HZ1	18:R:204:GLU:HA	1.35	0.92
1:A:684:ASP:OD2	8:H:20:TYR:HB3	1.69	0.92
1:A:1604:GLU:O	1:A:1612:LYS:HE2	1.70	0.92
16:P:184:SER:CB	18:R:198:LEU:H	1.83	0.92
1:A:403:LEU:O	1:A:406:LEU:HG	1.70	0.91
1:A:1317:ILE:HG21	1:A:1460:TYR:CE1	2.01	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1326:GLU:CD	1:A:1454:HIS:CA	2.38	0.91
2:B:548:LYS:HE3	2:B:695:ASN:OD1	1.70	0.91
1:A:435:ASN:CB	1:A:442:LYS:CB	2.49	0.91
1:A:1049:MET:HB3	1:A:1052:GLY:H	1.35	0.91
2:B:64:GLY:HA2	2:B:242:ASP:CB	2.00	0.91
6:F:66:ARG:NH2	7:G:90:LEU:HD12	1.85	0.91
7:G:159:LYS:HB3	15:O:105:ASN:HD22	1.34	0.91
16:P:354:PRO:HG3	18:R:31:PHE:CD2	2.05	0.91
2:B:152:LEU:HB3	2:B:443:LYS:HE2	1.50	0.91
20:Q:1002:SO4:O4	18:R:1:MET:N	2.03	0.91
15:O:248:LEU:CD1	15:O:598:PHE:HE2	1.54	0.91
1:A:990:ILE:HG13	1:A:995:TYR:H	1.35	0.91
2:B:1151:ILE:HG12	7:G:21:LYS:HZ2	1.35	0.91
16:P:436:ILE:CB	18:R:143:THR:HG23	1.99	0.91
1:A:436:ALA:CB	1:A:443:ALA:HB2	2.00	0.91
1:A:545:SER:HB3	17:Q:34:VAL:CG2	1.96	0.91
1:A:634:ASN:ND2	2:B:1069:ILE:HG21	1.85	0.91
1:A:862:THR:HB	9:I:67:VAL:HG12	1.50	0.91
1:A:878:ARG:CB	9:I:67:VAL:HG13	1.97	0.91
17:Q:15:CYS:CB	17:Q:16:PRO:HA	1.99	0.91
17:Q:356:VAL:CG1	18:R:208:TYR:CD1	2.52	0.91
1:A:425:ASN:ND2	18:R:405:ILE:HG21	1.84	0.91
1:A:995:TYR:OH	2:B:715:ASN:ND2	2.04	0.91
2:B:894:LYS:HG3	12:L:54:ARG:HH22	0.74	0.91
1:A:429:THR:CG2	18:R:406:LYS:HZ1	1.83	0.91
1:A:670:ILE:HG12	2:B:783:MET:CE	2.01	0.91
1:A:878:ARG:CD	9:I:66:VAL:HG21	2.00	0.91
2:B:266:LYS:CE	2:B:473:GLN:O	2.19	0.91
1:A:1313:LEU:CG	1:A:1462:PHE:CZ	2.54	0.90
15:O:247:GLU:OE1	15:O:325:ILE:HA	1.71	0.90
1:A:407:GLN:HE21	1:A:407:GLN:H	0.94	0.90
3:C:272:LYS:CG	14:N:175:TYR:CE1	2.54	0.90
18:R:173:MET:HG3	18:R:188:PHE:HZ	1.36	0.90
18:R:201:SER:O	18:R:205:VAL:CG2	2.20	0.90
16:P:434:ARG:N	18:R:145:SER:HA	1.85	0.90
18:R:199:LYS:CD	18:R:204:GLU:HB3	2.00	0.90
1:A:486:PRO:O	2:B:781:TYR:CE2	2.25	0.90
1:A:507:TYR:CE1	1:A:508:PRO:O	2.24	0.90
2:B:548:LYS:HE3	2:B:695:ASN:CG	1.92	0.90
18:R:202:THR:HA	18:R:205:VAL:HG21	1.52	0.90
18:R:203:SER:CA	20:R:601:SO4:O3	2.18	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:470:HIS:HD2	2:B:1058:GLN:OE1	1.54	0.90
1:A:579:ARG:HH12	1:A:581:ILE:HA	1.34	0.90
17:Q:3:THR:HG22	17:Q:20:TRP:HB2	1.53	0.90
17:Q:351:ASN:CG	17:Q:369:TRP:CZ2	2.45	0.90
1:A:438:ILE:O	1:A:457:LYS:HB2	1.72	0.90
15:O:247:GLU:OE1	15:O:325:ILE:CB	2.20	0.90
16:P:443:ASP:HB3	18:R:3:GLU:OE2	1.72	0.90
1:A:1326:GLU:OE1	1:A:1455:ARG:N	2.03	0.90
1:A:826:PHE:CD1	2:B:777:SER:HB2	2.07	0.90
1:A:878:ARG:HD2	9:I:66:VAL:HG21	1.54	0.90
16:P:390:GLN:O	18:R:150:GLN:N	2.04	0.90
1:A:408:LYS:CA	1:A:411:VAL:HB	2.02	0.89
3:C:274:THR:HA	14:N:172:ALA:HB2	0.90	0.89
17:Q:19:LEU:HD11	17:Q:27:ARG:HB3	1.54	0.89
2:B:551:ILE:CG2	2:B:647:SER:HA	2.02	0.89
1:A:436:ALA:HB2	1:A:443:ALA:CB	2.01	0.89
2:B:679:GLN:CG	14:N:156:PRO:CA	2.43	0.89
2:B:1092:LEU:CA	2:B:1096:SER:HB2	2.02	0.89
16:P:694:ILE:HB	16:P:746:ARG:HD3	1.54	0.89
17:Q:188:ALA:HB3	17:Q:384:GLN:HB3	1.55	0.89
17:Q:341:ARG:CZ	17:Q:369:TRP:HE1	1.85	0.89
1:A:474:LYS:HZ1	2:B:1092:LEU:CD2	1.82	0.89
16:P:248:PRO:HD2	16:P:267:ASN:HB3	1.54	0.89
18:R:202:THR:HA	18:R:205:VAL:CG2	2.02	0.89
16:P:197:ARG:HE	16:P:261:VAL:H	1.16	0.89
1:A:581:ILE:HG13	1:A:585:ASP:OD2	1.71	0.89
1:A:1314:GLN:OE1	1:A:1446:ARG:HD2	1.73	0.89
6:F:70:LYS:CD	7:G:95:LEU:HD23	2.01	0.89
1:A:40:ASN:OD1	18:R:355:THR:CG2	2.20	0.89
1:A:474:LYS:HZ1	2:B:1092:LEU:HD22	1.34	0.89
1:A:627:ASP:O	2:B:784:ASP:HB3	1.73	0.89
18:R:5:PRO:HG2	18:R:217:THR:HG21	0.89	0.89
1:A:403:LEU:CD1	1:A:419:ILE:CG2	2.45	0.89
1:A:435:ASN:O	1:A:439:ASP:CB	2.21	0.89
7:G:144:HIS:NE2	15:O:145:SER:CB	2.34	0.89
1:A:1314:GLN:HE22	1:A:1446:ARG:CD	1.83	0.89
2:B:64:GLY:HA2	2:B:242:ASP:HB3	1.54	0.89
15:O:376:TYR:CE1	15:O:588:LEU:HD21	2.07	0.89
14:N:86:ASP:O	14:N:141:GLU:HG2	1.71	0.89
1:A:990:ILE:HD12	1:A:994:GLU:C	1.92	0.88
1:A:1310:LYS:CG	1:A:1311:GLU:CD	2.26	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:534:PRO:HA	2:B:720:GLN:OE1	1.73	0.88
17:Q:193:PHE:O	18:R:209:ARG:NH1	2.06	0.88
2:B:1002:LYS:HD3	14:N:166:LEU:C	1.93	0.88
3:C:272:LYS:CG	14:N:175:TYR:CD1	2.56	0.88
1:A:413:LEU:O	1:A:416:ARG:HG2	1.73	0.88
16:P:433:VAL:HA	18:R:145:SER:CB	2.03	0.88
2:B:75:ASP:N	2:B:440:PHE:CE2	2.41	0.88
7:G:241:ARG:NH1	15:O:189:PHE:CB	2.35	0.88
3:C:58:ASN:HA	3:C:296:ASN:HD22	1.38	0.88
6:F:70:LYS:HD3	7:G:95:LEU:HD23	1.53	0.88
15:O:373:LEU:O	15:O:376:TYR:CB	2.21	0.88
1:A:1482:LYS:CD	2:B:304:ASP:OD1	2.22	0.88
2:B:800:TYR:OH	2:B:908:ARG:NH2	2.07	0.88
3:C:229:LEU:O	3:C:293:ARG:NH1	2.07	0.88
1:A:579:ARG:NH1	1:A:581:ILE:HA	1.88	0.88
2:B:145:VAL:CG1	2:B:441:LYS:HG2	2.04	0.88
18:R:199:LYS:CE	18:R:204:GLU:HA	2.03	0.88
1:A:543:LEU:O	17:Q:34:VAL:O	1.92	0.88
15:O:234:ILE:CG2	15:O:237:ILE:CG1	2.31	0.88
18:R:4:VAL:CG2	18:R:214:VAL:HG13	2.04	0.88
18:R:6:ILE:CD1	18:R:213:ILE:CB	2.50	0.88
1:A:1263:LEU:HA	1:A:1498:ILE:HD11	1.53	0.88
2:B:1151:ILE:HG12	7:G:21:LYS:NZ	1.88	0.88
16:P:397:LYS:NZ	18:R:85:ARG:HH11	1.50	0.88
1:A:1322:ILE:CG2	1:A:1454:HIS:NE2	2.37	0.88
2:B:26:ILE:O	10:J:62:ARG:NH1	2.05	0.88
1:A:436:ALA:O	1:A:439:ASP:C	2.11	0.87
1:A:547:ILE:CG1	17:Q:26:ARG:HH22	1.87	0.87
16:P:197:ARG:HD2	16:P:261:VAL:N	1.89	0.87
1:A:634:ASN:HD21	2:B:1069:ILE:HG21	1.37	0.87
1:A:954:GLY:N	1:A:1205:PHE:CB	2.37	0.87
1:A:998:HIS:O	2:B:712:SER:OG	1.92	0.87
1:A:1484:LEU:CD1	2:B:305:ARG:NE	2.35	0.87
3:C:293:ARG:H	3:C:295:ARG:NH1	1.72	0.87
1:A:474:LYS:HZ2	2:B:1092:LEU:HD23	1.34	0.87
1:A:1317:ILE:HG22	1:A:1460:TYR:CE1	2.09	0.87
17:Q:29:CYS:SG	17:Q:33:HIS:HB2	2.15	0.87
1:A:1053:ASP:O	1:A:1055:ILE:HG12	1.73	0.87
17:Q:12:THR:CB	17:Q:33:HIS:ND1	2.37	0.87
1:A:966:LEU:HD21	1:A:997:PHE:CE1	2.09	0.87
1:A:474:LYS:HZ3	2:B:1096:SER:CB	1.88	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:Q:20:TRP:CH2	17:Q:22:ILE:CG2	2.56	0.87
15:O:376:TYR:CZ	15:O:377:TYR:CZ	2.63	0.87
15:O:376:TYR:HE1	15:O:588:LEU:HD22	1.38	0.87
1:A:953:GLU:C	1:A:1205:PHE:CB	2.42	0.87
1:A:1085:LEU:HD22	6:F:84:TYR:OH	1.74	0.87
17:Q:378:LEU:HD23	18:R:216:LEU:HD21	1.56	0.87
1:A:1484:LEU:HD23	2:B:304:ASP:HB3	1.56	0.87
7:G:159:LYS:N	15:O:105:ASN:HD21	1.50	0.87
7:G:159:LYS:CA	15:O:105:ASN:ND2	2.38	0.87
2:B:149:GLU:OE1	2:B:441:LYS:CE	2.23	0.86
15:O:243:GLU:OE1	15:O:328:LEU:CD2	2.08	0.86
16:P:389:TRP:CH2	18:R:149:LYS:N	2.42	0.86
1:A:1314:GLN:NE2	1:A:1446:ARG:CZ	2.38	0.86
11:K:66:VAL:HG12	11:K:67:GLU:HG2	1.57	0.86
15:O:238:ILE:O	15:O:242:VAL:HG23	1.75	0.86
18:R:168:ILE:HG23	18:R:169:PRO:HD3	1.58	0.86
1:A:408:LYS:HA	1:A:411:VAL:HB	1.55	0.86
2:B:143:TRP:CE2	2:B:446:MET:CG	2.58	0.86
6:F:74:ILE:O	7:G:95:LEU:HD13	1.72	0.86
1:A:954:GLY:N	1:A:1205:PHE:HB2	1.90	0.86
1:A:995:TYR:CE2	2:B:708:ASP:CA	2.56	0.86
1:A:995:TYR:HH	2:B:707:SER:HB2	1.05	0.86
1:A:1056:ASP:HA	1:A:1179:ILE:HD13	1.57	0.86
15:O:200:ASN:CG	17:Q:14:ASN:CG	2.34	0.86
16:P:389:TRP:HH2	18:R:148:ASN:H	1.19	0.86
17:Q:409:ALA:O	17:Q:413:LEU:HB2	1.74	0.86
3:C:37:LYS:O	11:K:134:LYS:NZ	2.09	0.86
1:A:478:TYR:CD1	2:B:1048:SER:O	2.29	0.86
1:A:613:THR:HG21	2:B:913:ILE:HG21	1.57	0.86
1:A:756:LYS:CG	9:I:85:LYS:NZ	2.38	0.86
1:A:1650:GLY:C	1:A:1652:GLY:H	1.79	0.86
2:B:527:PHE:HZ	2:B:666:PRO:HA	1.39	0.86
3:C:230:LEU:HD12	3:C:231:PRO:CD	2.04	0.86
1:A:436:ALA:CA	1:A:439:ASP:O	2.24	0.86
3:C:293:ARG:N	3:C:295:ARG:NH1	2.23	0.86
1:A:40:ASN:ND2	18:R:355:THR:HG22	1.89	0.86
1:A:1326:GLU:OE2	1:A:1454:HIS:CA	2.24	0.86
17:Q:20:TRP:CZ3	17:Q:22:ILE:HG21	2.08	0.86
16:P:397:LYS:HZ2	18:R:85:ARG:NH1	1.71	0.86
16:P:438:TRP:CG	18:R:141:TRP:CZ2	2.62	0.86
1:A:1330:VAL:HG21	1:A:1455:ARG:NE	1.91	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:1089:GLN:CG	2:B:1093:LEU:HB2	2.06	0.85
16:P:436:ILE:HB	18:R:143:THR:HA	1.58	0.85
18:R:201:SER:O	18:R:205:VAL:HG23	1.75	0.85
1:A:756:LYS:CG	9:I:85:LYS:HZ2	1.89	0.85
1:A:1322:ILE:HD12	1:A:1457:ILE:HD12	1.57	0.85
2:B:143:TRP:CE2	2:B:446:MET:CB	2.58	0.85
16:P:184:SER:HB3	18:R:198:LEU:CA	2.07	0.85
2:B:849:GLY:HA3	12:L:60:ARG:NH2	1.89	0.85
6:F:72:LYS:CB	6:F:142:SER:HB2	2.05	0.85
1:A:477:ASN:ND2	2:B:1049:THR:OG1	2.09	0.85
1:A:1032:VAL:HG21	1:A:1050:TYR:CD1	2.11	0.85
1:A:1660:VAL:O	7:G:102:GLU:HA	1.74	0.85
2:B:143:TRP:CE2	2:B:446:MET:HG3	2.11	0.85
1:A:475:ARG:HB3	2:B:1059:PRO:HB2	1.57	0.85
1:A:1262:LEU:CD2	1:A:1497:ILE:HG12	2.06	0.85
1:A:1313:LEU:HD23	1:A:1462:PHE:HZ	1.38	0.85
7:G:144:HIS:ND1	15:O:146:SER:OG	2.10	0.85
16:P:397:LYS:CE	18:R:85:ARG:HD3	2.04	0.85
1:A:566:SER:HB2	15:O:235:GLU:OE2	1.73	0.85
1:A:990:ILE:HD12	1:A:994:GLU:O	1.77	0.85
1:A:1313:LEU:CD2	1:A:1462:PHE:HZ	1.88	0.85
2:B:399:HIS:O	2:B:400:GLN:HG2	1.77	0.85
17:Q:26:ARG:CB	17:Q:34:VAL:CG1	2.53	0.85
1:A:535:GLN:HE22	17:Q:26:ARG:HD3	1.06	0.84
3:C:322:LYS:HE3	11:K:129:ASP:OD1	1.77	0.84
18:R:251:TRP:CD2	18:R:307:LYS:HE3	2.11	0.84
15:O:181:ARG:HB2	15:O:181:ARG:HH11	1.41	0.84
1:A:475:ARG:NH2	2:B:1061:LYS:HB2	1.91	0.84
2:B:346:ASP:OD1	13:M:113:ILE:HG23	1.76	0.84
1:A:1032:VAL:HG21	1:A:1050:TYR:CE1	2.12	0.84
7:G:141:SER:HB3	15:O:142:ILE:HD11	1.59	0.84
7:G:241:ARG:NH1	15:O:189:PHE:HB3	1.92	0.84
15:O:240:ILE:CG2	15:O:380:SER:CB	2.42	0.84
15:O:247:GLU:OE1	15:O:325:ILE:CA	2.25	0.84
17:Q:413:LEU:CG	18:R:273:TRP:HZ2	1.90	0.84
2:B:346:ASP:H	13:M:113:ILE:HG12	1.40	0.84
2:B:1049:THR:HG23	2:B:1050:GLY:N	1.92	0.84
13:M:61:GLU:OE2	13:M:106:LYS:CE	2.13	0.84
2:B:894:LYS:CD	12:L:47:ARG:NE	2.40	0.84
1:A:399:LEU:HD21	1:A:423:LEU:HG	1.59	0.84
1:A:475:ARG:CZ	2:B:1061:LYS:CB	2.56	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:429:THR:CG2	18:R:406:LYS:NZ	2.40	0.84
7:G:241:ARG:HH11	15:O:189:PHE:HB3	1.40	0.84
1:A:564:PRO:CG	15:O:370:THR:O	2.25	0.84
18:R:5:PRO:HG3	18:R:217:THR:HB	0.84	0.84
1:A:1322:ILE:HG21	1:A:1454:HIS:CE1	2.08	0.84
2:B:1069:ILE:O	2:B:1070:ARG:HB3	1.76	0.84
17:Q:193:PHE:CE2	18:R:208:TYR:CD2	2.66	0.84
18:R:362:ALA:HB2	18:R:421:LYS:HB3	1.59	0.84
1:A:458:GLN:O	1:A:462:LYS:CB	2.26	0.83
1:A:1276:THR:C	9:I:44:ASN:HA	1.99	0.83
2:B:894:LYS:CG	12:L:54:ARG:CZ	2.56	0.83
2:B:985:ILE:HB	14:N:160:VAL:HG21	1.59	0.83
3:C:59:ILE:O	3:C:296:ASN:HB2	1.78	0.83
13:M:102:SER:CB	13:M:105:SER:H	1.90	0.83
15:O:200:ASN:HB2	17:Q:14:ASN:HA	1.58	0.83
16:P:185:GLN:HB3	18:R:195:LEU:CB	2.08	0.83
1:A:429:THR:HG21	18:R:406:LYS:HE3	0.86	0.83
1:A:718:THR:O	8:H:98:TYR:N	2.11	0.83
2:B:25:PHE:CE1	10:J:59:LYS:HD2	2.13	0.83
2:B:1089:GLN:CB	2:B:1093:LEU:HD22	2.09	0.83
1:A:999:CYS:HA	2:B:712:SER:HB3	1.57	0.83
1:A:629:ASP:OD1	2:B:926:VAL:HG23	1.79	0.83
1:A:1655:ASP:HB2	6:F:135:ARG:HB3	1.58	0.83
2:B:985:ILE:HB	14:N:160:VAL:HG22	1.59	0.83
2:B:743:ARG:NH2	10:J:60:PHE:HZ	1.71	0.83
2:B:864:ASP:HB3	17:Q:412:LYS:CE	2.07	0.83
15:O:584:GLN:OE1	15:O:584:GLN:N	2.11	0.83
16:P:389:TRP:HH2	18:R:148:ASN:CA	1.91	0.83
17:Q:15:CYS:HB3	17:Q:16:PRO:C	1.98	0.83
2:B:848:ILE:CA	12:L:60:ARG:HD2	2.08	0.83
2:B:1092:LEU:HA	2:B:1096:SER:CB	2.09	0.83
7:G:144:HIS:NE2	15:O:145:SER:C	2.31	0.83
17:Q:101:LYS:HG2	17:Q:152:LEU:HD11	1.58	0.83
1:A:966:LEU:CD2	1:A:997:PHE:CE1	2.61	0.83
2:B:623:ASP:O	2:B:648:ARG:NH1	2.10	0.83
2:B:1002:LYS:HD2	14:N:166:LEU:CB	2.09	0.83
15:O:245:GLN:NE2	15:O:379:ARG:HB2	1.93	0.83
16:P:390:GLN:O	18:R:149:LYS:C	2.17	0.83
1:A:938:VAL:CG2	9:I:82:ILE:HD13	2.07	0.83
2:B:119:ARG:CZ	12:L:53:HIS:CE1	2.61	0.83
2:B:207:ILE:HD11	2:B:503:VAL:CG2	2.03	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:679:GLN:CD	14:N:157:ARG:HA	1.99	0.83
2:B:682:GLN:HA	14:N:154:ARG:NH2	1.92	0.83
6:F:74:ILE:O	7:G:95:LEU:HD12	1.79	0.83
15:O:181:ARG:HH11	15:O:181:ARG:CB	1.89	0.83
18:R:199:LYS:NZ	18:R:204:GLU:HA	1.93	0.83
1:A:672:ASP:OD1	2:B:777:SER:OG	1.96	0.83
16:P:397:LYS:HZ1	18:R:85:ARG:HH11	1.01	0.83
1:A:473:GLY:HA2	2:B:1072:GLY:HA2	1.60	0.82
1:A:544:VAL:HG13	17:Q:32:GLY:O	1.79	0.82
1:A:966:LEU:CD2	1:A:997:PHE:CZ	2.62	0.82
2:B:266:LYS:HE3	2:B:473:GLN:C	1.99	0.82
1:A:756:LYS:HD3	9:I:85:LYS:HZ2	1.37	0.82
1:A:1297:PHE:CE2	9:I:60:LEU:HD22	2.13	0.82
16:P:323:ASN:HA	16:P:350:THR:HA	1.61	0.82
17:Q:15:CYS:HB3	17:Q:16:PRO:HA	1.60	0.82
1:A:503:VAL:CA	1:A:580:HIS:HD2	1.69	0.82
1:A:506:THR:CA	1:A:579:ARG:O	2.26	0.82
18:R:15:GLN:CD	18:R:184:ASN:ND2	2.29	0.82
1:A:429:THR:HG21	18:R:406:LYS:NZ	1.93	0.82
1:A:478:TYR:CG	2:B:1048:SER:O	2.33	0.82
1:A:535:GLN:NE2	17:Q:26:ARG:CD	2.34	0.82
2:B:550:ARG:O	2:B:649:MET:HA	1.79	0.82
2:B:894:LYS:O	2:B:896:GLN:N	2.11	0.82
1:A:615:ARG:NH1	2:B:929:ARG:NE	2.28	0.82
16:P:397:LYS:HE3	18:R:85:ARG:CZ	2.10	0.82
16:P:398:ALA:HB2	18:R:87:VAL:HA	1.61	0.82
1:A:435:ASN:CB	1:A:442:LYS:HB3	2.08	0.82
1:A:472:MET:HE2	1:A:472:MET:HA	1.61	0.82
1:A:615:ARG:NH2	2:B:929:ARG:HG2	1.94	0.82
2:B:889:GLY:CA	12:L:54:ARG:O	2.28	0.82
3:C:334:THR:CG2	11:K:44:ARG:HB3	2.09	0.82
7:G:159:LYS:H	15:O:105:ASN:CG	1.82	0.82
16:P:397:LYS:HE2	18:R:85:ARG:HE	1.41	0.82
17:Q:351:ASN:CB	17:Q:369:TRP:CZ2	2.62	0.82
18:R:317:LEU:CD1	18:R:367:ILE:CD1	2.58	0.82
2:B:776:ILE:HB	2:B:1026:ILE:HD13	1.60	0.82
2:B:850:THR:N	12:L:60:ARG:HH22	1.78	0.82
16:P:185:GLN:CB	18:R:195:LEU:HB3	2.10	0.82
13:M:102:SER:HB3	13:M:105:SER:CA	2.09	0.82
16:P:394:VAL:HG11	18:R:144:VAL:CG2	2.10	0.82
1:A:407:GLN:HB3	1:A:409:ASP:H	1.43	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:679:GLN:CD	14:N:157:ARG:CA	2.48	0.82
6:F:73:ALA:HA	6:F:143:PHE:O	1.80	0.82
2:B:49:PHE:CE2	2:B:194:PHE:CZ	2.68	0.81
13:M:102:SER:O	13:M:105:SER:C	2.17	0.81
16:P:185:GLN:HA	18:R:196:GLU:C	1.99	0.81
17:Q:188:ALA:HB1	17:Q:384:GLN:HG3	1.61	0.81
18:R:252:GLY:O	18:R:256:GLU:HB2	1.79	0.81
1:A:824:THR:O	2:B:1023:ARG:N	2.12	0.81
2:B:864:ASP:HB3	17:Q:412:LYS:HE3	1.62	0.81
16:P:397:LYS:HE2	18:R:85:ARG:CD	2.04	0.81
1:A:535:GLN:HE21	17:Q:26:ARG:HD3	1.44	0.81
1:A:545:SER:CB	17:Q:34:VAL:HG23	2.08	0.81
2:B:566:TYR:HB3	13:M:74:ASN:OD1	1.79	0.81
2:B:975:HIS:ND1	14:N:169:GLU:HG3	1.96	0.81
6:F:72:LYS:CB	6:F:142:SER:CA	2.24	0.81
16:P:472:ARG:NE	18:R:200:THR:CG2	2.43	0.81
17:Q:20:TRP:HZ3	17:Q:22:ILE:HG22	0.65	0.81
18:R:206:ARG:H	18:R:206:ARG:HE	1.26	0.81
18:R:206:ARG:NH2	18:R:211:ARG:HH11	1.78	0.81
1:A:828:CYS:HB3	2:B:1027:TYR:HB2	1.60	0.81
1:A:1603:MET:HE2	1:A:1615:TYR:CD2	2.15	0.81
2:B:610:TYR:HE1	2:B:658:LEU:HD11	1.44	0.81
18:R:426:VAL:HG12	18:R:428:SER:H	1.45	0.81
1:A:422:ARG:NH1	18:R:412:ARG:CZ	2.42	0.81
6:F:70:LYS:HG2	7:G:95:LEU:HG	1.62	0.81
6:F:72:LYS:HD3	6:F:142:SER:HB3	1.61	0.81
15:O:248:LEU:CD1	15:O:598:PHE:HD2	1.52	0.81
16:P:185:GLN:HG3	18:R:190:SER:CB	2.10	0.81
14:N:87:TYR:CB	14:N:141:GLU:HA	1.93	0.81
1:A:984:GLY:N	1:A:994:GLU:OE2	2.13	0.81
1:A:1180:ASN:OD1	6:F:87:LYS:CD	2.25	0.81
1:A:1276:THR:OG1	9:I:45:LEU:HD13	1.77	0.81
2:B:29:PRO:HB2	2:B:177:PRO:HG2	1.62	0.81
6:F:74:ILE:C	7:G:95:LEU:HD11	2.00	0.81
1:A:480:ALA:HB2	2:B:1046:VAL:HG23	1.60	0.81
1:A:547:ILE:HD11	17:Q:26:ARG:CZ	1.90	0.81
1:A:670:ILE:CG1	2:B:783:MET:HE2	2.10	0.81
2:B:567:SER:O	14:N:140:SER:HB3	1.81	0.81
3:C:272:LYS:CB	14:N:175:TYR:CE1	2.64	0.81
15:O:240:ILE:HG22	15:O:380:SER:HB2	1.58	0.81
17:Q:198:ILE:HG21	17:Q:388:THR:CG2	2.11	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:R:251:TRP:HE3	18:R:307:LYS:HE3	1.31	0.81
1:A:1575:ILE:CB	9:I:122:ARG:NH1	2.44	0.81
7:G:24:VAL:HG11	7:G:126:GLN:NE2	1.95	0.81
15:O:376:TYR:CE1	15:O:419:LYS:HE2	2.15	0.81
17:Q:20:TRP:CE3	17:Q:22:ILE:HG23	2.15	0.81
1:A:1482:LYS:HD2	2:B:307:GLU:OE1	1.81	0.80
2:B:794:ASP:OD1	2:B:911:PRO:HD2	1.81	0.80
15:O:342:HIS:CE1	15:O:346:GLN:HE21	1.98	0.80
17:Q:188:ALA:CB	17:Q:384:GLN:HB3	2.10	0.80
1:A:954:GLY:CA	1:A:1205:PHE:CB	2.59	0.80
1:A:40:ASN:HD21	18:R:355:THR:HG22	1.44	0.80
1:A:477:ASN:C	2:B:1047:ARG:HD3	2.01	0.80
1:A:990:ILE:O	1:A:992:PRO:N	2.14	0.80
14:N:87:TYR:HA	14:N:141:GLU:HA	0.81	0.80
15:O:235:GLU:O	15:O:238:ILE:HD12	1.81	0.80
1:A:425:ASN:ND2	18:R:406:LYS:HZ2	1.78	0.80
1:A:1329:ILE:CG2	1:A:1456:PHE:CZ	2.64	0.80
2:B:75:ASP:HB3	2:B:440:PHE:CD2	2.15	0.80
2:B:208:VAL:HG23	2:B:401:GLU:HG2	1.64	0.80
2:B:1003:ALA:O	14:N:170:HIS:CA	2.29	0.80
14:N:87:TYR:CE2	14:N:141:GLU:OE1	2.34	0.80
16:P:472:ARG:CZ	18:R:200:THR:CG2	2.58	0.80
1:A:477:ASN:HA	2:B:1047:ARG:NH1	1.95	0.80
1:A:478:TYR:O	1:A:479:ALA:HB2	1.79	0.80
1:A:721:LYS:NZ	8:H:91:ASP:HA	1.96	0.80
1:A:1657:LEU:HB2	6:F:133:VAL:HB	1.62	0.80
16:P:184:SER:CB	18:R:198:LEU:CB	2.39	0.80
15:O:201:LYS:HD2	15:O:239:SER:OG	1.82	0.80
16:P:390:GLN:O	18:R:149:LYS:HB3	1.80	0.80
16:P:436:ILE:O	18:R:141:TRP:O	2.00	0.80
1:A:862:THR:HG22	9:I:67:VAL:CG1	2.10	0.80
12:L:34:CYS:HB3	12:L:51:CYS:SG	2.21	0.80
1:A:407:GLN:CB	1:A:409:ASP:H	1.94	0.80
1:A:719:ILE:HG12	8:H:97:MET:HG2	1.62	0.80
1:A:1575:ILE:CA	9:I:122:ARG:NH1	2.43	0.80
2:B:681:ILE:HB	14:N:154:ARG:CG	2.12	0.80
16:P:349:GLY:CA	18:R:153:ASN:O	2.30	0.80
1:A:1330:VAL:CG2	1:A:1455:ARG:NE	2.44	0.80
3:C:272:LYS:HA	14:N:175:TYR:CE2	2.14	0.80
7:G:141:SER:HB2	15:O:142:ILE:CD1	1.95	0.80
16:P:473:HIS:CD2	18:R:1:MET:CB	2.10	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:862:THR:HA	9:I:67:VAL:CB	2.12	0.80
2:B:551:ILE:HA	2:B:648:ARG:O	1.82	0.80
2:B:796:ARG:HD2	10:J:8:PHE:HA	1.62	0.80
7:G:159:LYS:H	15:O:105:ASN:HD21	0.80	0.80
1:A:581:ILE:HD12	1:A:637:PHE:CE1	2.17	0.79
1:A:1038:ILE:HD11	1:A:1050:TYR:HA	1.64	0.79
1:A:1120:TYR:O	5:E:207:ARG:NH2	2.12	0.79
2:B:25:PHE:O	10:J:62:ARG:HD2	1.83	0.79
1:A:990:ILE:CD1	1:A:995:TYR:CA	2.60	0.79
16:P:321:LYS:H	16:P:321:LYS:HD3	1.46	0.79
17:Q:371:GLU:HG3	18:R:231:LEU:HD12	1.62	0.79
1:A:1310:LYS:HD3	1:A:1310:LYS:H	1.45	0.79
2:B:49:PHE:CE2	2:B:194:PHE:HZ	2.01	0.79
18:R:347:ASP:O	18:R:351:GLU:HB2	1.81	0.79
1:A:472:MET:HG3	2:B:1073:GLU:OE1	1.82	0.79
3:C:272:LYS:N	14:N:175:TYR:CE1	2.35	0.79
16:P:397:LYS:HZ1	18:R:85:ARG:CD	1.79	0.79
16:P:434:ARG:H	18:R:145:SER:HA	1.44	0.79
17:Q:17:SER:O	17:Q:29:CYS:CB	2.30	0.79
18:R:317:LEU:CD1	18:R:367:ILE:HD13	2.12	0.79
16:P:198:ASP:HB3	16:P:205:TYR:O	1.79	0.79
17:Q:351:ASN:CA	17:Q:369:TRP:HH2	1.93	0.79
1:A:476:VAL:HG22	2:B:1070:ARG:N	1.97	0.79
2:B:697:LEU:HB2	2:B:702:ASN:CG	2.03	0.79
2:B:68:ILE:HG23	2:B:71:LYS:NZ	1.84	0.79
13:M:102:SER:C	13:M:105:SER:H	1.86	0.79
16:P:185:GLN:CA	18:R:196:GLU:O	2.28	0.79
17:Q:188:ALA:CB	17:Q:384:GLN:HG3	2.12	0.79
17:Q:356:VAL:HG11	18:R:208:TYR:HD1	1.45	0.79
7:G:144:HIS:HD2	15:O:146:SER:HA	1.42	0.79
17:Q:356:VAL:CG1	18:R:212:HIS:CE1	2.66	0.79
1:A:425:ASN:ND2	18:R:406:LYS:NZ	2.30	0.79
1:A:671:GLN:OE1	2:B:952:HIS:HB2	1.83	0.79
1:A:721:LYS:HB3	8:H:96:VAL:HB	1.64	0.79
14:N:88:LYS:N	14:N:140:SER:O	2.15	0.79
1:A:1049:MET:HG3	1:A:1053:ASP:N	1.97	0.79
2:B:532:HIS:NE2	2:B:723:LYS:NZ	2.31	0.79
3:C:272:LYS:CA	14:N:175:TYR:CD1	2.44	0.79
16:P:775:TRP:H	17:Q:109:GLN:HE22	1.28	0.79
1:A:399:LEU:HD23	1:A:423:LEU:HD23	1.63	0.78
1:A:532:GLY:C	1:A:580:HIS:HD1	1.86	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:547:ILE:HG13	17:Q:26:ARG:HH22	1.48	0.78
3:C:103:LEU:O	10:J:6:ARG:NE	2.12	0.78
6:F:66:ARG:NH2	7:G:90:LEU:HD13	1.98	0.78
2:B:143:TRP:CZ2	2:B:446:MET:HA	2.18	0.78
2:B:1093:LEU:CG	2:B:1094:ASN:OD1	2.29	0.78
1:A:407:GLN:HE21	1:A:407:GLN:N	1.78	0.78
1:A:1657:LEU:HD23	7:G:104:LEU:HB3	1.65	0.78
6:F:66:ARG:HH22	7:G:90:LEU:CD1	1.94	0.78
17:Q:356:VAL:HG13	18:R:212:HIS:HE1	1.48	0.78
1:A:620:ASN:OD1	1:A:667:ARG:NH2	2.17	0.78
1:A:862:THR:HA	9:I:67:VAL:HA	1.65	0.78
1:A:1298:ASP:HA	1:A:1468:LYS:HZ3	1.49	0.78
2:B:145:VAL:HG11	2:B:441:LYS:CG	2.09	0.78
3:C:253:PRO:CD	14:N:180:PHE:HD1	1.90	0.78
16:P:434:ARG:HG2	18:R:143:THR:CB	2.13	0.78
18:R:317:LEU:HD12	18:R:367:ILE:CD1	2.13	0.78
1:A:83:VAL:HG11	1:A:427:PHE:CZ	2.19	0.78
1:A:88:PRO:HG3	1:A:434:VAL:HG12	1.65	0.78
1:A:403:LEU:HD11	1:A:419:ILE:HG21	0.85	0.78
1:A:862:THR:HA	9:I:67:VAL:CA	2.13	0.78
1:A:1049:MET:CG	1:A:1052:GLY:CA	2.62	0.78
2:B:75:ASP:CB	2:B:440:PHE:CZ	2.66	0.78
2:B:119:ARG:NH2	12:L:53:HIS:CE1	2.52	0.78
2:B:679:GLN:CG	14:N:156:PRO:HA	2.14	0.78
18:R:199:LYS:CE	18:R:203:SER:C	2.52	0.78
1:A:478:TYR:O	1:A:479:ALA:CB	2.29	0.78
1:A:996:TYR:CE2	2:B:530:PRO:HG3	2.19	0.78
18:R:177:LEU:HD22	18:R:185:LYS:HG2	1.66	0.78
1:A:1049:MET:HG2	1:A:1052:GLY:CA	2.13	0.78
2:B:184:LYS:HB3	2:B:735:HIS:ND1	1.99	0.78
1:A:435:ASN:O	1:A:439:ASP:C	2.21	0.78
1:A:672:ASP:CG	2:B:777:SER:HB3	2.04	0.77
1:A:1032:VAL:CG2	1:A:1050:TYR:CD1	2.67	0.77
1:A:1600:ARG:NE	1:A:1616:GLU:OE1	2.16	0.77
17:Q:351:ASN:HA	17:Q:369:TRP:CH2	2.19	0.77
15:O:376:TYR:CG	15:O:419:LYS:HE2	2.19	0.77
1:A:547:ILE:HD13	17:Q:26:ARG:NH1	1.98	0.77
1:A:566:SER:CB	15:O:235:GLU:OE1	2.28	0.77
1:A:1484:LEU:CD2	2:B:304:ASP:HB3	2.14	0.77
2:B:679:GLN:CG	14:N:155:VAL:O	2.32	0.77
15:O:186:SER:O	15:O:190:ILE:HG22	1.85	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:207:ILE:HG12	2:B:503:VAL:HG21	1.61	0.77
2:B:878:GLU:OE2	2:B:909:ARG:NH1	2.17	0.77
2:B:143:TRP:CH2	2:B:446:MET:HA	2.19	0.77
16:P:245:ILE:HG12	16:P:269:PHE:HB2	1.66	0.77
16:P:405:TYR:CE1	16:P:414:ILE:HG23	2.19	0.77
18:R:248:LYS:HG2	18:R:298:GLN:CD	2.05	0.77
1:A:878:ARG:CB	9:I:67:VAL:HG11	2.05	0.77
2:B:73:ILE:HD12	2:B:425:ILE:HG23	1.67	0.77
2:B:743:ARG:NH2	10:J:60:PHE:CE2	2.52	0.77
15:O:155:SER:HA	15:O:158:LEU:HD12	1.67	0.77
17:Q:358:PRO:CB	18:R:206:ARG:NH1	2.47	0.77
1:A:407:GLN:H	1:A:407:GLN:NE2	1.79	0.77
2:B:566:TYR:HD2	13:M:73:SER:HG	1.21	0.77
3:C:326:GLU:HG3	11:K:125:MET:HE1	1.66	0.77
17:Q:12:THR:OG1	17:Q:33:HIS:ND1	2.17	0.77
1:A:1326:GLU:CD	1:A:1454:HIS:C	2.39	0.77
2:B:46:ILE:HA	2:B:164:MET:SD	2.25	0.77
7:G:144:HIS:CD2	15:O:146:SER:OG	2.38	0.77
7:G:159:LYS:HB2	15:O:105:ASN:ND2	1.95	0.77
15:O:235:GLU:O	15:O:238:ILE:CD1	2.33	0.77
16:P:397:LYS:HZ3	18:R:85:ARG:CD	1.80	0.77
1:A:990:ILE:HG13	1:A:995:TYR:CA	2.14	0.77
2:B:1096:SER:O	2:B:1097:ASP:HB3	1.84	0.77
1:A:953:GLU:O	1:A:1205:PHE:CG	2.38	0.76
2:B:415:GLU:OE2	2:B:474:SER:OG	2.02	0.76
15:O:435:SER:OG	15:O:438:GLN:HG3	1.84	0.76
1:A:991:LYS:N	1:A:994:GLU:CG	2.30	0.76
2:B:207:ILE:HD11	2:B:503:VAL:HG11	1.66	0.76
2:B:1003:ALA:O	14:N:170:HIS:HB3	1.85	0.76
16:P:200:THR:HG21	16:P:280:ARG:NH1	1.99	0.76
2:B:527:PHE:CD2	2:B:666:PRO:HB3	2.19	0.76
1:A:986:PHE:HE2	2:B:958:MET:HE1	1.50	0.76
2:B:346:ASP:N	13:M:113:ILE:HG12	1.99	0.76
1:A:382:GLN:HE21	1:A:456:VAL:HG22	1.50	0.76
1:A:1484:LEU:HD23	2:B:304:ASP:CB	2.15	0.76
8:H:80:ARG:HG3	11:K:108:TYR:CZ	2.21	0.76
16:P:24:SER:CB	18:R:318:ILE:HD11	2.14	0.76
1:A:475:ARG:NH2	2:B:1061:LYS:CG	2.49	0.76
3:C:142:ARG:CZ	10:J:67:GLU:OE2	2.33	0.76
3:C:315:PHE:CE2	11:K:139:ILE:HD12	2.20	0.76
7:G:144:HIS:CG	15:O:146:SER:CB	2.69	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:P:436:ILE:H	18:R:143:THR:N	1.84	0.76
1:A:493:ASN:HB3	1:A:654:ASP:OD1	1.85	0.76
1:A:1657:LEU:N	6:F:133:VAL:O	2.17	0.76
2:B:563:SER:CB	13:M:73:SER:HB3	2.16	0.76
2:B:679:GLN:CD	14:N:157:ARG:N	2.39	0.76
16:P:598:LEU:HD23	16:P:601:ARG:HD2	1.68	0.76
2:B:1089:GLN:CG	2:B:1093:LEU:CD1	2.59	0.76
1:A:409:ASP:OD1	1:A:410:LYS:N	2.19	0.76
1:A:1204:THR:HG21	9:I:97:HIS:HB3	1.66	0.76
2:B:202:LEU:HD11	2:B:499:HIS:HB3	1.67	0.76
6:F:70:LYS:O	6:F:74:ILE:N	2.19	0.76
1:A:435:ASN:CB	1:A:442:LYS:HB2	2.11	0.76
1:A:581:ILE:HD12	1:A:637:PHE:CZ	2.21	0.75
15:O:62:ASP:HB3	15:O:67:ASP:OD2	1.86	0.75
17:Q:22:ILE:HD11	17:Q:24:ASP:OD2	1.86	0.75
18:R:414:PHE:HA	18:R:417:ILE:HG22	1.66	0.75
16:P:197:ARG:CD	16:P:261:VAL:N	2.49	0.75
16:P:398:ALA:CB	18:R:87:VAL:HA	2.16	0.75
18:R:180:CYS:O	18:R:185:LYS:HE3	1.86	0.75
2:B:527:PHE:CZ	2:B:666:PRO:N	2.54	0.75
7:G:144:HIS:CD2	15:O:146:SER:N	2.55	0.75
16:P:698:LYS:HE2	17:Q:124:ARG:HH21	1.50	0.75
17:Q:22:ILE:CG1	17:Q:24:ASP:OD2	2.34	0.75
1:A:953:GLU:CG	1:A:1205:PHE:CE2	2.69	0.75
2:B:551:ILE:HG23	2:B:648:ARG:H	1.48	0.75
15:O:248:LEU:HD11	15:O:598:PHE:CD2	1.86	0.75
1:A:670:ILE:CG1	2:B:783:MET:CE	2.65	0.75
1:A:1603:MET:CE	1:A:1615:TYR:CD2	2.69	0.75
1:A:472:MET:HA	1:A:472:MET:CE	2.16	0.75
1:A:990:ILE:CG1	1:A:994:GLU:HB2	2.16	0.75
1:A:1298:ASP:O	1:A:1301:GLU:N	2.20	0.75
3:C:253:PRO:HD2	14:N:180:PHE:HB3	0.78	0.75
16:P:443:ASP:HB3	18:R:3:GLU:CB	2.17	0.75
1:A:408:LYS:HB2	1:A:411:VAL:HB	1.68	0.75
1:A:474:LYS:H	2:B:1070:ARG:HG3	1.51	0.75
2:B:527:PHE:CZ	2:B:666:PRO:CB	2.70	0.75
7:G:143:SER:HB2	15:O:104:ILE:CB	2.15	0.75
1:A:40:ASN:CG	18:R:355:THR:CG2	2.55	0.74
15:O:376:TYR:OH	15:O:588:LEU:CD2	2.35	0.74
16:P:438:TRP:HD1	18:R:141:TRP:CZ2	1.98	0.74
1:A:1313:LEU:CG	1:A:1462:PHE:HZ	1.99	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:474:LYS:NZ	2:B:1096:SER:CB	2.49	0.74
2:B:518:ARG:NH2	2:B:537:SER:O	2.21	0.74
1:A:425:ASN:ND2	18:R:405:ILE:CG2	2.50	0.74
1:A:984:GLY:CA	1:A:994:GLU:OE2	2.36	0.74
1:A:991:LYS:CB	1:A:993:GLN:CB	2.62	0.74
1:A:999:CYS:HA	2:B:712:SER:OG	1.86	0.74
1:A:1049:MET:HG2	1:A:1052:GLY:O	1.84	0.74
2:B:1005:TYR:CE2	14:N:170:HIS:CG	2.75	0.74
16:P:384:ASP:HB3	16:P:389:TRP:HB3	1.69	0.74
17:Q:3:THR:O	17:Q:20:TRP:HB3	1.87	0.74
17:Q:417:PHE:HZ	18:R:270:PHE:CD1	2.05	0.74
1:A:406:LEU:HB3	1:A:408:LYS:H	1.53	0.74
1:A:629:ASP:O	2:B:926:VAL:HG21	1.87	0.74
1:A:1322:ILE:CG2	1:A:1454:HIS:ND1	2.24	0.74
2:B:25:PHE:O	10:J:62:ARG:CD	2.35	0.74
2:B:679:GLN:HG2	14:N:157:ARG:CA	2.14	0.74
2:B:1089:GLN:CD	2:B:1093:LEU:HD13	2.07	0.74
1:A:1050:TYR:HB3	1:A:1054:ALA:HA	1.69	0.74
1:A:1314:GLN:CD	1:A:1446:ARG:CD	2.56	0.74
6:F:72:LYS:C	6:F:143:PHE:H	1.91	0.74
13:M:102:SER:CB	13:M:105:SER:N	2.49	0.74
15:O:379:ARG:HA	15:O:379:ARG:NH1	1.99	0.74
17:Q:198:ILE:HG21	17:Q:388:THR:HG23	1.69	0.74
1:A:1487:ASN:OD1	2:B:305:ARG:NH2	2.21	0.74
3:C:100:ARG:NH2	10:J:3:VAL:O	2.20	0.74
13:M:102:SER:C	13:M:105:SER:N	2.40	0.74
16:P:389:TRP:CA	18:R:151:PRO:HA	2.17	0.74
17:Q:410:ARG:HA	17:Q:413:LEU:HB3	1.69	0.74
1:A:615:ARG:HH21	2:B:781:TYR:HD2	1.36	0.74
1:A:921:PRO:HD3	8:H:19:ARG:HG2	1.68	0.74
1:A:952:LEU:CD2	1:A:1004:GLU:HG3	2.07	0.74
7:G:142:ALA:CB	15:O:102:SER:O	2.35	0.74
16:P:480:VAL:HB	16:P:492:LEU:HD21	1.68	0.74
1:A:588:LEU:CD2	2:B:1087:LEU:HD13	2.18	0.74
3:C:322:LYS:CE	11:K:129:ASP:OD1	2.35	0.74
15:O:579:LEU:CA	15:O:582:ARG:HB3	2.11	0.74
1:A:40:ASN:CG	18:R:355:THR:HG22	2.08	0.73
1:A:1650:GLY:C	1:A:1652:GLY:N	2.38	0.73
2:B:1003:ALA:O	14:N:170:HIS:CB	2.36	0.73
15:O:373:LEU:HB3	15:O:374:PRO:HD3	1.69	0.73
1:A:399:LEU:CD2	1:A:423:LEU:HD23	2.18	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:824:THR:CB	2:B:1023:ARG:HB2	2.11	0.73
2:B:497:ILE:HG12	2:B:699:ILE:HD13	1.68	0.73
7:G:241:ARG:NH1	15:O:189:PHE:HB2	1.95	0.73
16:P:436:ILE:HB	18:R:143:THR:CA	2.17	0.73
17:Q:22:ILE:CD1	17:Q:26:ARG:CZ	2.65	0.73
18:R:5:PRO:HD2	18:R:217:THR:OG1	1.86	0.73
1:A:40:ASN:OD1	18:R:355:THR:HG22	1.88	0.73
2:B:146:ASN:HD22	2:B:441:LYS:HE3	1.53	0.73
7:G:143:SER:CB	15:O:104:ILE:CG2	2.17	0.73
1:A:1204:THR:CG2	9:I:97:HIS:HB3	2.17	0.73
2:B:152:LEU:HB3	2:B:443:LYS:HE3	0.73	0.73
16:P:200:THR:HG21	16:P:280:ARG:HH11	1.54	0.73
1:A:878:ARG:CG	9:I:67:VAL:CG1	2.55	0.73
1:A:1329:ILE:HG22	1:A:1456:PHE:CZ	2.22	0.73
2:B:73:ILE:HB	2:B:425:ILE:HD12	1.70	0.73
15:O:243:GLU:CB	15:O:332:LEU:HD13	2.17	0.73
15:O:245:GLN:HA	15:O:245:GLN:HE21	1.51	0.73
1:A:435:ASN:O	1:A:439:ASP:CA	2.37	0.73
1:A:472:MET:HE2	2:B:1076:ARG:HD3	1.68	0.73
1:A:998:HIS:NE2	2:B:711:GLN:CG	2.50	0.73
2:B:346:ASP:CG	13:M:113:ILE:HG23	2.07	0.73
2:B:401:GLU:HG3	2:B:402:VAL:N	2.03	0.73
6:F:72:LYS:O	6:F:143:PHE:N	2.20	0.73
15:O:202:ASN:CB	17:Q:31:TYR:OH	2.34	0.73
16:P:357:LEU:HG	18:R:24:ILE:HD11	1.69	0.73
1:A:403:LEU:CD1	1:A:419:ILE:HD13	2.18	0.73
1:A:1262:LEU:HD21	1:A:1497:ILE:HG12	1.69	0.73
2:B:346:ASP:OD2	13:M:114:LYS:N	2.22	0.73
2:B:399:HIS:O	2:B:400:GLN:CG	2.35	0.73
7:G:143:SER:CB	15:O:104:ILE:CB	2.66	0.73
1:A:399:LEU:CD2	1:A:423:LEU:CD2	2.67	0.73
1:A:435:ASN:C	1:A:439:ASP:O	2.27	0.73
1:A:481:ARG:O	2:B:1045:GLN:O	2.06	0.73
2:B:894:LYS:HG3	12:L:54:ARG:CZ	2.15	0.73
2:B:1092:LEU:O	2:B:1096:SER:CB	2.36	0.73
1:A:1310:LYS:HB3	1:A:1464:ASP:O	1.88	0.73
16:P:389:TRP:CZ2	18:R:147:GLN:HA	2.23	0.73
16:P:446:ASP:OD2	16:P:448:THR:HG22	1.89	0.73
1:A:436:ALA:O	1:A:440:SER:CA	2.37	0.73
2:B:184:LYS:HD3	2:B:735:HIS:NE2	2.04	0.73
2:B:527:PHE:CE1	2:B:666:PRO:CA	2.72	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:1151:ILE:HG23	7:G:21:LYS:HG3	1.70	0.73
18:R:206:ARG:HH21	18:R:211:ARG:HH11	1.34	0.73
1:A:618:TYR:CE1	2:B:783:MET:HB2	2.24	0.72
1:A:1658:ALA:HA	6:F:131:PRO:O	1.88	0.72
6:F:72:LYS:HD2	6:F:142:SER:HB3	0.76	0.72
16:P:322:GLY:O	16:P:350:THR:OG1	2.07	0.72
2:B:25:PHE:CD2	10:J:59:LYS:HG3	2.24	0.72
17:Q:15:CYS:CB	17:Q:16:PRO:CA	2.62	0.72
17:Q:288:GLU:O	17:Q:290:THR:OG1	2.06	0.72
18:R:199:LYS:HE3	18:R:203:SER:C	2.08	0.72
18:R:373:LEU:HD12	18:R:411:VAL:HG21	1.70	0.72
2:B:26:ILE:O	10:J:62:ARG:CZ	2.36	0.72
2:B:566:TYR:CE2	13:M:70:SER:HA	2.24	0.72
1:A:953:GLU:HG2	1:A:1205:PHE:HE2	1.54	0.72
2:B:143:TRP:HB3	2:B:446:MET:SD	2.29	0.72
16:P:197:ARG:NE	16:P:261:VAL:N	2.34	0.72
16:P:436:ILE:O	18:R:141:TRP:CD2	2.43	0.72
2:B:345:SER:HA	13:M:113:ILE:CG1	2.17	0.72
16:P:214:LEU:HB3	16:P:220:THR:HB	1.71	0.72
1:A:984:GLY:HA3	1:A:994:GLU:CD	2.09	0.72
1:A:1329:ILE:HB	1:A:1456:PHE:HE2	1.54	0.72
17:Q:12:THR:OG1	17:Q:33:HIS:CE1	2.42	0.72
1:A:474:LYS:HZ2	2:B:1092:LEU:CA	1.97	0.72
1:A:629:ASP:CA	2:B:926:VAL:HG21	2.19	0.72
2:B:527:PHE:CE1	2:B:666:PRO:N	2.58	0.72
1:A:1329:ILE:HG21	1:A:1456:PHE:CZ	2.24	0.72
2:B:683:ASN:H	14:N:154:ARG:NH2	1.86	0.72
2:B:843:ASP:OD2	12:L:58:LYS:NZ	2.23	0.72
2:B:1121:GLY:O	15:O:152:GLN:NE2	2.23	0.72
15:O:234:ILE:HG23	15:O:237:ILE:CG1	2.06	0.72
16:P:656:HIS:H	16:P:656:HIS:CD2	2.06	0.72
18:R:5:PRO:CD	18:R:217:THR:HG21	2.19	0.72
2:B:184:LYS:HD3	2:B:735:HIS:CD2	2.25	0.72
15:O:216:LEU:HD13	15:O:342:HIS:CG	2.25	0.72
16:P:662:LEU:HB3	16:P:665:ASN:ND2	2.05	0.72
18:R:4:VAL:CG1	18:R:214:VAL:HG22	2.20	0.72
1:A:990:ILE:CD1	1:A:995:TYR:N	2.52	0.71
1:A:1310:LYS:HD3	1:A:1310:LYS:N	2.05	0.71
1:A:1554:GLY:HA2	5:E:183:PRO:HD2	1.72	0.71
3:C:231:PRO:HB2	3:C:270:ALA:HB1	1.72	0.71
9:I:2:SER:HB2	9:I:11:LEU:HD21	1.72	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:P:348:HIS:NE2	18:R:154:LYS:HD3	2.04	0.71
17:Q:418:PRO:HD2	18:R:233:TYR:OH	1.90	0.71
1:A:478:TYR:HA	2:B:1048:SER:C	2.10	0.71
1:A:952:LEU:HD22	1:A:1004:GLU:CG	2.09	0.71
1:A:1660:VAL:O	7:G:102:GLU:CG	2.37	0.71
2:B:182:GLN:O	10:J:69:ARG:NE	2.23	0.71
16:P:186:TYR:N	18:R:196:GLU:O	2.23	0.71
16:P:434:ARG:HB3	18:R:143:THR:HB	1.69	0.71
17:Q:351:ASN:HA	17:Q:369:TRP:CZ2	2.24	0.71
17:Q:358:PRO:C	18:R:206:ARG:HH12	1.92	0.71
1:A:984:GLY:HA3	1:A:994:GLU:OE2	1.89	0.71
15:O:200:ASN:CA	17:Q:14:ASN:HB2	2.15	0.71
2:B:30:LYS:C	2:B:176:SER:HB2	2.11	0.71
16:P:184:SER:CA	18:R:198:LEU:CB	2.67	0.71
17:Q:288:GLU:HG3	17:Q:297:ARG:HH12	1.55	0.71
1:A:40:ASN:OD1	18:R:355:THR:HG23	1.89	0.71
1:A:990:ILE:CD1	1:A:994:GLU:C	2.57	0.71
1:A:999:CYS:CA	2:B:712:SER:HB3	2.15	0.71
2:B:1089:GLN:NE2	2:B:1093:LEU:HD13	2.05	0.71
3:C:296:ASN:OD1	3:C:297:HIS:N	2.24	0.71
1:A:953:GLU:O	1:A:1205:PHE:CD1	2.43	0.71
2:B:1069:ILE:HD12	2:B:1069:ILE:N	2.06	0.71
15:O:66:ASN:HD22	15:O:66:ASN:N	1.89	0.71
16:P:438:TRP:CD1	18:R:141:TRP:CE2	2.79	0.71
1:A:524:ILE:O	1:A:554:ARG:NH1	2.24	0.71
2:B:898:LEU:N	12:L:46:VAL:HG21	2.06	0.71
3:C:31:TRP:CH2	11:K:127:LEU:HD12	2.26	0.71
15:O:200:ASN:HD22	17:Q:14:ASN:C	1.92	0.71
15:O:348:THR:CG2	15:O:351:SER:HB3	2.19	0.71
16:P:532:GLU:HA	16:P:554:ASN:HD22	1.55	0.71
18:R:173:MET:HG3	18:R:188:PHE:CZ	2.25	0.71
1:A:543:LEU:CB	17:Q:34:VAL:O	2.38	0.71
6:F:75:PRO:HG3	6:F:78:GLN:CD	2.11	0.71
1:A:83:VAL:CG1	1:A:427:PHE:CZ	2.73	0.71
2:B:207:ILE:CD1	2:B:503:VAL:HG22	2.21	0.71
2:B:345:SER:HA	13:M:113:ILE:HD11	1.72	0.71
2:B:527:PHE:CE1	2:B:666:PRO:CD	2.73	0.71
2:B:1165:ASN:N	2:B:1165:ASN:OD1	2.24	0.71
3:C:272:LYS:HA	14:N:175:TYR:CG	2.24	0.71
16:P:22:GLY:HA2	18:R:139:GLU:OE2	1.89	0.71
16:P:364:GLU:O	16:P:373:LEU:HB2	1.91	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1482:LYS:HD3	2:B:304:ASP:OD1	1.90	0.70
1:A:1299:ASN:OD1	1:A:1467:GLY:C	2.28	0.70
1:A:1309:SER:HB2	1:A:1310:LYS:HD3	1.71	0.70
1:A:1657:LEU:HD22	7:G:104:LEU:HD12	1.70	0.70
3:C:230:LEU:HD13	3:C:299:ILE:HD11	1.72	0.70
13:M:38:PHE:HB3	13:M:53:LEU:HD11	1.73	0.70
16:P:375:PHE:CE1	16:P:380:MET:HG3	2.26	0.70
17:Q:183:LYS:O	17:Q:187:THR:OG1	2.08	0.70
18:R:6:ILE:CD1	18:R:213:ILE:HG22	2.16	0.70
1:A:475:ARG:NH2	2:B:1061:LYS:HG3	2.06	0.70
13:M:102:SER:O	13:M:105:SER:OG	2.08	0.70
16:P:390:GLN:CA	18:R:150:GLN:O	2.39	0.70
1:A:474:LYS:O	2:B:1070:ARG:CG	2.39	0.70
1:A:507:TYR:CE1	1:A:509:GLU:HA	2.26	0.70
1:A:862:THR:CG2	9:I:67:VAL:HG12	2.21	0.70
1:A:986:PHE:CE2	2:B:958:MET:HE1	2.26	0.70
2:B:1049:THR:HG23	2:B:1050:GLY:H	1.56	0.70
18:R:5:PRO:CD	18:R:217:THR:CG2	2.67	0.70
1:A:629:ASP:HA	2:B:926:VAL:CG2	2.21	0.70
1:A:909:SER:HA	9:I:83:LYS:HZ3	1.56	0.70
1:A:1246:VAL:O	1:A:1517:ARG:NH2	2.24	0.70
2:B:1072:GLY:CA	2:B:1075:GLU:CG	2.63	0.70
14:N:87:TYR:CB	14:N:141:GLU:CA	2.65	0.70
16:P:345:ASP:OD1	16:P:345:ASP:N	2.23	0.70
16:P:658:LYS:HB3	16:P:660:LYS:H	1.55	0.70
2:B:679:GLN:HG2	14:N:157:ARG:H	0.87	0.70
14:N:87:TYR:CA	14:N:141:GLU:CA	2.45	0.70
1:A:436:ALA:C	1:A:439:ASP:N	2.32	0.70
1:A:543:LEU:C	17:Q:34:VAL:O	2.30	0.70
1:A:921:PRO:HD2	8:H:19:ARG:HG3	1.73	0.70
2:B:75:ASP:CA	2:B:440:PHE:CE2	2.74	0.70
2:B:894:LYS:HG2	12:L:47:ARG:NE	2.07	0.70
2:B:894:LYS:HA	12:L:54:ARG:NE	2.06	0.70
16:P:197:ARG:CD	16:P:261:VAL:H	2.04	0.70
16:P:659:LEU:H	16:P:659:LEU:HD13	1.55	0.70
17:Q:22:ILE:CD1	17:Q:26:ARG:HE	2.04	0.70
2:B:143:TRP:CZ2	2:B:446:MET:CB	2.75	0.70
2:B:207:ILE:HD11	2:B:503:VAL:CG1	2.20	0.70
7:G:142:ALA:HB3	15:O:102:SER:O	1.92	0.70
1:A:613:THR:CG2	2:B:913:ILE:HG21	2.21	0.70
2:B:527:PHE:CE2	2:B:666:PRO:CA	2.62	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:548:LYS:CE	2:B:695:ASN:OD1	2.40	0.70
16:P:390:GLN:HB2	18:R:151:PRO:C	2.13	0.70
17:Q:351:ASN:C	17:Q:369:TRP:HH2	1.95	0.70
1:A:921:PRO:CD	8:H:19:ARG:HG2	2.22	0.70
2:B:291:GLY:HA3	2:B:375:LEU:HD13	1.74	0.70
1:A:489:ASN:HB2	11:K:95:HIS:CD2	2.27	0.69
2:B:65:VAL:HG23	2:B:417:ILE:HD12	1.74	0.69
2:B:999:GLN:HG2	14:N:166:LEU:HD13	1.73	0.69
2:B:1069:ILE:HD12	2:B:1069:ILE:H	1.57	0.69
16:P:292:LEU:HD11	16:P:343:LEU:HG	1.72	0.69
16:P:443:ASP:C	18:R:3:GLU:HB2	2.09	0.69
1:A:65:CYS:SG	19:A:2001:ZN:ZN	1.81	0.69
1:A:99:ARG:O	1:A:109:ARG:NH2	2.24	0.69
1:A:399:LEU:HD23	1:A:423:LEU:CD2	2.21	0.69
1:A:1313:LEU:HG	1:A:1462:PHE:HE1	1.49	0.69
2:B:203:ILE:CG2	2:B:405:GLY:CA	2.71	0.69
18:R:199:LYS:HE2	18:R:203:SER:C	2.11	0.69
1:A:475:ARG:NE	2:B:1061:LYS:HB2	2.06	0.69
1:A:1313:LEU:CD2	1:A:1462:PHE:CZ	2.72	0.69
2:B:212:ASN:ND2	2:B:361:HIS:HB2	2.08	0.69
2:B:848:ILE:HG22	12:L:60:ARG:NH1	2.07	0.69
16:P:382:GLU:OE1	18:R:146:SER:OG	2.10	0.69
16:P:405:TYR:HB2	16:P:416:LEU:HD12	1.73	0.69
17:Q:22:ILE:HD12	17:Q:24:ASP:CG	2.11	0.69
17:Q:188:ALA:CB	17:Q:384:GLN:HG2	2.09	0.69
1:A:686:PHE:HZ	8:H:121:LEU:HD11	1.56	0.69
1:A:862:THR:CA	9:I:67:VAL:HA	2.21	0.69
2:B:143:TRP:CG	2:B:446:MET:HE3	2.23	0.69
2:B:475:GLY:O	2:B:476:LEU:HB2	1.92	0.69
16:P:584:ARG:O	16:P:588:SER:HB2	1.91	0.69
1:A:828:CYS:CB	2:B:1027:TYR:HB2	2.21	0.69
15:O:376:TYR:CD1	15:O:419:LYS:CE	2.74	0.69
16:P:218:VAL:HG13	16:P:246:LYS:H	1.57	0.69
17:Q:8:PRO:HG2	17:Q:19:LEU:HD23	1.75	0.69
1:A:507:TYR:HE1	1:A:509:GLU:HA	1.56	0.69
1:A:990:ILE:C	1:A:994:GLU:HB2	2.12	0.69
2:B:143:TRP:CZ2	2:B:446:MET:HB2	2.28	0.69
2:B:212:ASN:HD21	2:B:361:HIS:HB2	1.56	0.69
3:C:31:TRP:HH2	11:K:127:LEU:HD12	1.58	0.69
15:O:248:LEU:CG	15:O:598:PHE:CE2	2.74	0.69
15:O:376:TYR:CD1	15:O:419:LYS:CD	2.76	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:P:412:ASN:OD1	16:P:412:ASN:N	2.24	0.69
1:A:953:GLU:CB	1:A:1205:PHE:CE2	2.75	0.69
2:B:404:LEU:O	2:B:407:PHE:N	2.23	0.69
2:B:850:THR:N	12:L:60:ARG:NH2	2.40	0.69
16:P:302:VAL:HG21	16:P:362:ARG:HD2	1.75	0.69
17:Q:186:CYS:O	18:R:208:TYR:OH	2.10	0.69
18:R:201:SER:O	18:R:205:VAL:HG22	1.90	0.69
2:B:679:GLN:CG	14:N:157:ARG:CA	2.70	0.69
4:D:99:LEU:HB3	4:D:100:PRO:CD	2.22	0.69
16:P:301:GLN:HG3	16:P:361:LYS:H	1.57	0.69
16:P:302:VAL:HG11	16:P:362:ARG:HH11	1.57	0.69
16:P:389:TRP:HA	18:R:151:PRO:HA	1.74	0.69
16:P:428:GLU:HB2	16:P:435:ARG:HH12	1.58	0.69
16:P:472:ARG:NE	18:R:200:THR:HG23	2.07	0.69
1:A:862:THR:O	9:I:66:VAL:O	2.10	0.69
1:A:480:ALA:HB1	2:B:1046:VAL:HG23	1.74	0.68
1:A:862:THR:C	9:I:67:VAL:HA	2.13	0.68
2:B:887:LEU:HB2	12:L:56:LEU:O	1.93	0.68
6:F:75:PRO:HG2	6:F:78:GLN:CB	2.08	0.68
15:O:233:LEU:O	15:O:236:LYS:HB2	1.94	0.68
16:P:24:SER:OG	18:R:318:ILE:HG13	1.93	0.68
16:P:232:ASN:N	16:P:232:ASN:OD1	2.27	0.68
16:P:389:TRP:HZ2	18:R:147:GLN:HA	1.57	0.68
1:A:1298:ASP:CG	1:A:1468:LYS:NZ	2.46	0.68
2:B:143:TRP:CD1	2:B:446:MET:SD	2.84	0.68
6:F:70:LYS:CG	7:G:95:LEU:HG	2.22	0.68
17:Q:22:ILE:HG13	17:Q:24:ASP:OD2	1.92	0.68
1:A:502:ALA:O	1:A:580:HIS:HB3	1.93	0.68
1:A:646:GLU:OE2	2:B:1086:PHE:HD2	1.75	0.68
1:A:1330:VAL:CG2	1:A:1455:ARG:NH1	2.56	0.68
2:B:266:LYS:CD	2:B:473:GLN:O	2.40	0.68
2:B:864:ASP:HB3	17:Q:412:LYS:NZ	2.08	0.68
3:C:230:LEU:CD1	3:C:231:PRO:HD2	2.13	0.68
2:B:551:ILE:CG2	2:B:647:SER:CA	2.72	0.68
6:F:70:LYS:HG2	7:G:95:LEU:CD2	2.23	0.68
16:P:193:LEU:HD12	16:P:251:SER:H	1.59	0.68
1:A:406:LEU:HB2	1:A:408:LYS:HZ2	1.57	0.68
1:A:470:HIS:CD2	2:B:1058:GLN:OE1	2.43	0.68
2:B:49:PHE:CB	2:B:164:MET:CE	2.62	0.68
2:B:62:ASN:OD1	2:B:102:VAL:HG23	1.93	0.68
3:C:41:GLU:OE2	11:K:138:LYS:CE	2.41	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:R:359:MET:N	18:R:359:MET:SD	2.67	0.68
2:B:209:GLN:HG2	2:B:210:ARG:N	2.07	0.68
15:O:237:ILE:HD12	15:O:237:ILE:H	1.59	0.68
17:Q:414:TYR:HE1	18:R:240:ILE:HG23	1.55	0.68
2:B:985:ILE:CB	14:N:160:VAL:CG2	2.67	0.68
16:P:473:HIS:CD2	18:R:1:MET:CG	2.77	0.68
17:Q:341:ARG:CZ	17:Q:369:TRP:NE1	2.54	0.68
17:Q:418:PRO:CG	18:R:233:TYR:OH	2.42	0.68
1:A:466:LEU:HD11	2:B:1181:VAL:HG21	1.74	0.68
1:A:671:GLN:OE1	2:B:952:HIS:CB	2.42	0.68
2:B:985:ILE:C	14:N:160:VAL:HG23	2.14	0.68
15:O:237:ILE:HD12	15:O:237:ILE:N	2.08	0.68
16:P:53:ASP:OD2	16:P:54:ALA:N	2.27	0.68
3:C:125:LYS:O	3:C:130:ASN:ND2	2.27	0.68
7:G:144:HIS:CD2	15:O:146:SER:CB	2.77	0.68
15:O:248:LEU:HD12	15:O:598:PHE:HE2	0.87	0.68
17:Q:418:PRO:HG2	18:R:233:TYR:OH	1.93	0.68
1:A:475:ARG:CB	2:B:1059:PRO:HB2	2.24	0.67
1:A:991:LYS:HB3	1:A:993:GLN:CB	2.23	0.67
1:A:1660:VAL:HG22	7:G:103:LYS:O	1.93	0.67
16:P:197:ARG:CG	16:P:261:VAL:O	2.42	0.67
1:A:83:VAL:CG1	1:A:427:PHE:CE2	2.77	0.67
1:A:408:LYS:HA	1:A:411:VAL:CB	2.25	0.67
1:A:1314:GLN:HE22	1:A:1446:ARG:NE	1.91	0.67
3:C:127:THR:H	3:C:130:ASN:HB2	1.59	0.67
5:E:76:GLY:HA3	5:E:106:GLN:HB2	1.76	0.67
1:A:1310:LYS:H	1:A:1310:LYS:CD	2.08	0.67
1:A:1655:ASP:OD2	6:F:137:TYR:OH	2.10	0.67
6:F:66:ARG:HH21	7:G:90:LEU:CD1	2.06	0.67
15:O:200:ASN:CB	17:Q:14:ASN:CA	2.53	0.67
17:Q:193:PHE:CE2	18:R:208:TYR:CE2	2.82	0.67
7:G:242:VAL:HG21	15:O:183:ILE:HG23	1.74	0.67
18:R:199:LYS:HD3	18:R:204:GLU:HB3	1.76	0.67
1:A:472:MET:CE	2:B:1076:ARG:HD3	2.24	0.67
2:B:527:PHE:CE2	2:B:666:PRO:HB3	2.29	0.67
6:F:72:LYS:HA	6:F:142:SER:CB	2.13	0.67
13:M:102:SER:O	13:M:105:SER:CB	2.42	0.67
1:A:878:ARG:HB3	9:I:67:VAL:HG12	1.68	0.67
2:B:531:VAL:O	2:B:716:MET:HG3	1.95	0.67
2:B:985:ILE:CB	14:N:160:VAL:HG21	2.24	0.67
16:P:622:TYR:CZ	16:P:668:SER:HB3	2.30	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:R:161:ASN:HA	18:R:164:LYS:HD2	1.76	0.67
1:A:403:LEU:HD12	1:A:419:ILE:HD13	1.76	0.67
1:A:406:LEU:N	1:A:406:LEU:HD23	2.10	0.67
1:A:990:ILE:CG1	1:A:995:TYR:CA	2.72	0.67
1:A:1656:VAL:HA	6:F:133:VAL:O	1.95	0.67
16:P:458:LYS:HD3	16:P:461:HIS:HE1	1.60	0.67
17:Q:355:VAL:HB	18:R:212:HIS:CE1	2.30	0.67
1:A:477:ASN:HA	2:B:1047:ARG:HD3	1.77	0.67
1:A:799:GLU:HG3	1:A:1062:HIS:CE1	2.30	0.67
1:A:988:SER:HB2	2:B:988:GLU:HG2	1.76	0.67
2:B:679:GLN:HG3	14:N:156:PRO:HA	1.73	0.67
15:O:373:LEU:HD12	15:O:423:TYR:CE2	2.30	0.67
17:Q:198:ILE:HD13	17:Q:390:THR:O	1.95	0.67
18:R:4:VAL:HG11	18:R:214:VAL:HG22	1.75	0.67
1:A:545:SER:CB	17:Q:34:VAL:HG22	2.10	0.67
1:A:671:GLN:HB3	2:B:952:HIS:CD2	2.30	0.67
1:A:1484:LEU:CD2	2:B:304:ASP:CB	2.73	0.67
1:A:113:VAL:HG21	1:A:178:LEU:HD13	1.77	0.67
15:O:468:GLU:O	15:O:471:LYS:HG3	1.94	0.67
16:P:489:PHE:HD2	18:R:140:ILE:HD11	1.60	0.67
17:Q:139:LYS:HG2	17:Q:237:ILE:HG12	1.76	0.67
2:B:68:ILE:HG21	2:B:71:LYS:HZ3	0.60	0.66
3:C:272:LYS:CB	14:N:175:TYR:CD1	2.78	0.66
13:M:102:SER:CB	13:M:105:SER:CA	2.70	0.66
16:P:435:ARG:HH21	18:R:140:ILE:HG21	1.60	0.66
18:R:266:SER:O	18:R:269:ASP:N	2.28	0.66
1:A:1276:THR:CB	9:I:45:LEU:CD1	2.63	0.66
2:B:796:ARG:O	10:J:8:PHE:CE1	2.48	0.66
18:R:206:ARG:NH2	18:R:211:ARG:NH1	2.43	0.66
1:A:475:ARG:NH2	2:B:1061:LYS:CB	2.57	0.66
1:A:629:ASP:CA	2:B:926:VAL:CG2	2.72	0.66
1:A:1326:GLU:OE1	1:A:1454:HIS:C	2.34	0.66
2:B:202:LEU:HD22	2:B:488:ALA:CB	2.25	0.66
16:P:187:ILE:CG2	18:R:195:LEU:HD23	2.24	0.66
17:Q:378:LEU:HB3	18:R:238:THR:HG21	1.78	0.66
18:R:253:ILE:HA	18:R:256:GLU:HB3	1.76	0.66
2:B:848:ILE:HB	12:L:60:ARG:HD2	0.71	0.66
2:B:1002:LYS:CD	14:N:166:LEU:C	2.60	0.66
16:P:353:ASP:OD1	16:P:379:LYS:NZ	2.27	0.66
6:F:70:LYS:HG2	7:G:95:LEU:CG	2.26	0.66
18:R:186:LEU:O	18:R:186:LEU:HD13	1.95	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:399:LEU:HD21	1:A:423:LEU:CG	2.25	0.66
1:A:611:GLU:OE2	2:B:929:ARG:NH2	2.29	0.66
1:A:998:HIS:CE1	2:B:711:GLN:HG3	2.31	0.66
17:Q:196:SER:HB3	17:Q:204:ARG:HG2	1.76	0.66
15:O:233:LEU:O	15:O:237:ILE:CD1	2.35	0.66
16:P:394:VAL:HG11	18:R:144:VAL:HG23	1.78	0.66
1:A:435:ASN:CG	1:A:442:LYS:HB3	2.16	0.66
1:A:486:PRO:HG2	2:B:781:TYR:HA	1.78	0.66
1:A:966:LEU:CD2	1:A:997:PHE:HE1	2.09	0.66
7:G:144:HIS:CD2	15:O:145:SER:C	2.69	0.66
15:O:439:ILE:HD13	15:O:487:ARG:HD3	1.76	0.66
16:P:443:ASP:HB3	18:R:3:GLU:HB3	1.77	0.66
1:A:1032:VAL:CG2	1:A:1050:TYR:CE1	2.79	0.66
1:A:1032:VAL:CG2	1:A:1050:TYR:HD1	2.05	0.66
1:A:1330:VAL:CG2	1:A:1455:ARG:CD	2.73	0.66
16:P:321:LYS:HA	16:P:361:LYS:HD3	1.78	0.66
16:P:775:TRP:HE1	16:P:778:ASP:HA	1.61	0.66
17:Q:15:CYS:HB2	17:Q:16:PRO:HA	1.77	0.66
18:R:202:THR:CA	18:R:205:VAL:HG23	2.26	0.66
18:R:242:ILE:HG22	18:R:245:VAL:HG22	1.77	0.66
1:A:581:ILE:HG13	1:A:585:ASP:CG	2.15	0.66
1:A:990:ILE:HA	1:A:994:GLU:CD	2.15	0.66
1:A:1330:VAL:HG23	1:A:1455:ARG:NH1	2.10	0.66
2:B:469:ASN:OD1	2:B:482:SER:HB3	1.95	0.66
3:C:294:VAL:O	3:C:297:HIS:CB	2.44	0.66
16:P:448:THR:CG2	16:P:471:MET:H	2.08	0.66
1:A:109:ARG:NH1	1:A:230:ARG:O	2.29	0.65
1:A:506:THR:CG2	1:A:579:ARG:C	2.59	0.65
1:A:722:PRO:HD3	8:H:95:TYR:HA	1.76	0.65
1:A:953:GLU:HA	1:A:1205:PHE:HD2	1.52	0.65
2:B:711:GLN:HG2	2:B:713:PRO:HD2	1.78	0.65
4:D:99:LEU:HB3	4:D:100:PRO:HD3	1.78	0.65
15:O:245:GLN:CD	15:O:379:ARG:HB2	2.16	0.65
17:Q:15:CYS:SG	17:Q:17:SER:CB	2.83	0.65
17:Q:208:PRO:HG2	17:Q:211:TYR:HD2	1.59	0.65
1:A:718:THR:HG23	8:H:118:PHE:HB3	1.78	0.65
1:A:824:THR:O	2:B:1023:ARG:CB	2.44	0.65
1:A:1054:ALA:O	1:A:1179:ILE:HG22	1.97	0.65
15:O:238:ILE:HD12	15:O:238:ILE:H	1.61	0.65
1:A:627:ASP:O	2:B:784:ASP:O	2.15	0.65
1:A:862:THR:HA	9:I:67:VAL:HB	1.77	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:212:ASN:ND2	2:B:361:HIS:CB	2.59	0.65
2:B:527:PHE:CE1	2:B:666:PRO:CB	2.79	0.65
2:B:894:LYS:HG2	12:L:47:ARG:HE	1.62	0.65
15:O:108:GLU:HG3	15:O:108:GLU:O	1.96	0.65
1:A:1273:THR:HG23	9:I:48:VAL:HG22	1.79	0.65
2:B:209:GLN:O	2:B:401:GLU:N	2.27	0.65
2:B:1072:GLY:O	2:B:1075:GLU:N	2.29	0.65
7:G:144:HIS:CE1	15:O:145:SER:CB	2.79	0.65
1:A:467:PHE:CE2	1:A:1614:SER:HB3	2.31	0.65
1:A:615:ARG:NH2	2:B:781:TYR:CD2	2.64	0.65
16:P:389:TRP:CH2	18:R:148:ASN:CA	2.76	0.65
16:P:428:GLU:HB3	18:R:142:ARG:NH1	2.11	0.65
16:P:434:ARG:CB	18:R:143:THR:HB	2.25	0.65
17:Q:188:ALA:CB	17:Q:384:GLN:CB	2.64	0.65
17:Q:208:PRO:HG2	17:Q:211:TYR:CD2	2.31	0.65
1:A:474:LYS:NZ	2:B:1092:LEU:HD22	1.97	0.65
15:O:428:ILE:HD11	15:O:442:VAL:HG21	1.79	0.65
1:A:824:THR:HB	2:B:1023:ARG:CB	2.13	0.65
1:A:921:PRO:CD	8:H:19:ARG:CG	2.75	0.65
2:B:345:SER:HA	13:M:113:ILE:CD1	2.27	0.65
2:B:1072:GLY:O	2:B:1075:GLU:CA	2.45	0.65
3:C:292:GLY:HA3	3:C:295:ARG:NH2	2.12	0.65
1:A:1655:ASP:O	6:F:135:ARG:N	2.23	0.65
2:B:681:ILE:CB	14:N:154:ARG:HG3	2.23	0.65
2:B:990:ASP:OD1	14:N:162:LYS:NZ	2.23	0.65
16:P:656:HIS:HB2	16:P:747:LEU:O	1.97	0.65
16:P:769:GLN:HA	16:P:772:ILE:HB	1.79	0.65
17:Q:218:SER:O	17:Q:218:SER:OG	2.11	0.65
2:B:328:GLN:NE2	13:M:111:PRO:O	2.29	0.65
2:B:341:SER:OG	2:B:343:ASP:OD1	2.13	0.65
3:C:328:LEU:HD23	11:K:121:LEU:HD21	1.79	0.65
17:Q:26:ARG:HB3	17:Q:34:VAL:HG11	1.75	0.65
18:R:199:LYS:NZ	18:R:204:GLU:CB	2.60	0.65
2:B:49:PHE:CD2	2:B:194:PHE:HZ	2.14	0.65
2:B:152:LEU:CD2	2:B:443:LYS:HD2	2.15	0.65
2:B:399:HIS:C	2:B:400:GLN:CG	2.65	0.65
2:B:1090:ASP:O	2:B:1094:ASN:HB2	1.96	0.65
6:F:73:ALA:HA	6:F:143:PHE:CG	2.32	0.65
15:O:219:ARG:NH2	15:O:360:VAL:HG22	2.12	0.65
15:O:510:VAL:HG13	15:O:517:LEU:HD11	1.79	0.65
16:P:625:ASP:O	16:P:629:ARG:CB	2.45	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:Q:189:LYS:HA	17:Q:384:GLN:HE21	1.62	0.65
17:Q:417:PHE:HZ	18:R:270:PHE:HB2	1.61	0.65
1:A:671:GLN:HB3	2:B:952:HIS:CG	2.32	0.64
1:A:825:ALA:O	2:B:1023:ARG:NH1	2.30	0.64
1:A:436:ALA:HA	1:A:440:SER:HA	1.80	0.64
1:A:1659:LYS:HG2	7:G:102:GLU:OE1	1.98	0.64
2:B:679:GLN:HG3	14:N:155:VAL:C	2.16	0.64
16:P:197:ARG:HE	16:P:261:VAL:HG22	1.62	0.64
16:P:263:ILE:HG22	16:P:264:ILE:HG22	1.79	0.64
16:P:434:ARG:HG2	18:R:143:THR:HB	1.80	0.64
18:R:4:VAL:HG21	18:R:214:VAL:CG1	2.27	0.64
3:C:293:ARG:HB2	3:C:295:ARG:HD3	1.80	0.64
15:O:240:ILE:HA	15:O:332:LEU:HD12	1.79	0.64
16:P:775:TRP:H	17:Q:109:GLN:NE2	1.95	0.64
18:R:186:LEU:HD13	18:R:186:LEU:C	2.17	0.64
18:R:317:LEU:HD13	18:R:367:ILE:CD1	2.24	0.64
1:A:40:ASN:ND2	18:R:355:THR:CG2	2.59	0.64
1:A:460:LEU:HD21	2:B:1188:GLU:HG3	1.80	0.64
5:E:20:LYS:HE2	5:E:34:GLU:HG2	1.80	0.64
6:F:70:LYS:CE	7:G:95:LEU:HD23	2.26	0.64
15:O:240:ILE:HG23	15:O:332:LEU:HG	1.78	0.64
16:P:697:GLU:OE1	16:P:697:GLU:N	2.30	0.64
17:Q:15:CYS:HB3	17:Q:17:SER:H	1.62	0.64
18:R:303:THR:HG22	18:R:304:HIS:H	1.62	0.64
1:A:476:VAL:CA	2:B:1059:PRO:HG2	2.28	0.64
1:A:507:TYR:CD1	1:A:508:PRO:C	2.70	0.64
2:B:531:VAL:HG13	2:B:716:MET:HA	1.78	0.64
7:G:144:HIS:NE2	15:O:146:SER:N	2.46	0.64
15:O:376:TYR:CG	15:O:419:LYS:CE	2.80	0.64
16:P:736:ILE:HD11	17:Q:254:LEU:HD13	1.80	0.64
18:R:412:ARG:NH2	18:R:439:GLU:OE2	2.31	0.64
1:A:684:ASP:OD2	8:H:20:TYR:CB	2.45	0.64
2:B:551:ILE:CG2	2:B:648:ARG:N	2.58	0.64
16:P:405:TYR:OH	16:P:414:ILE:HG12	1.97	0.64
18:R:202:THR:O	18:R:205:VAL:HG23	1.97	0.64
1:A:641:GLU:HB2	6:F:99:LEU:HD13	1.78	0.64
2:B:923:GLN:NE2	2:B:953:ALA:O	2.30	0.64
15:O:392:GLN:HB2	15:O:395:LEU:HD22	1.79	0.64
16:P:436:ILE:CB	18:R:143:THR:HA	2.28	0.64
17:Q:104:PHE:CZ	17:Q:156:LEU:HB2	2.33	0.64
17:Q:245:SER:HB3	17:Q:284:LEU:HB2	1.80	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:Q:374:THR:HG23	18:R:219:LEU:HD13	1.80	0.64
1:A:720:PHE:CE2	8:H:141:TYR:CE2	2.78	0.64
16:P:434:ARG:H	18:R:145:SER:CA	2.10	0.64
17:Q:8:PRO:HB2	17:Q:19:LEU:HD23	1.79	0.64
17:Q:290:THR:HB	17:Q:292:GLU:H	1.61	0.64
18:R:1:MET:HE3	18:R:2:PHE:CE1	2.32	0.64
2:B:294:GLY:HA3	2:B:579:ALA:HB3	1.80	0.64
14:N:87:TYR:OH	14:N:141:GLU:OE1	2.16	0.64
15:O:396:MET:HE3	15:O:433:LYS:HB2	1.80	0.64
17:Q:20:TRP:CH2	17:Q:22:ILE:HG21	2.30	0.64
17:Q:378:LEU:CD2	18:R:216:LEU:HD21	2.27	0.64
1:A:998:HIS:CD2	2:B:711:GLN:HA	2.33	0.64
2:B:848:ILE:CB	12:L:60:ARG:CD	2.39	0.64
2:B:1005:TYR:CD2	14:N:170:HIS:ND1	2.66	0.64
7:G:143:SER:CB	15:O:104:ILE:N	2.49	0.64
18:R:4:VAL:HG21	18:R:214:VAL:HG13	1.78	0.64
1:A:406:LEU:HB3	1:A:408:LYS:HD3	1.80	0.63
3:C:229:LEU:CD2	3:C:295:ARG:O	2.42	0.63
15:O:227:PHE:HD1	15:O:363:THR:HB	1.62	0.63
16:P:700:LEU:HD12	16:P:703:PHE:HD2	1.62	0.63
1:A:684:ASP:OD1	8:H:20:TYR:HB3	1.97	0.63
2:B:1072:GLY:C	2:B:1075:GLU:H	2.02	0.63
2:B:1079:LEU:O	2:B:1083:GLY:N	2.31	0.63
7:G:144:HIS:CE1	15:O:145:SER:HB2	2.34	0.63
15:O:332:LEU:HD11	15:O:380:SER:CB	2.29	0.63
17:Q:283:ASN:OD1	17:Q:284:LEU:N	2.27	0.63
1:A:425:ASN:CG	18:R:406:LYS:NZ	2.46	0.63
1:A:1263:LEU:HA	1:A:1498:ILE:CD1	2.25	0.63
3:C:253:PRO:CD	14:N:180:PHE:CG	2.46	0.63
8:H:44:VAL:HG22	8:H:48:PRO:HA	1.81	0.63
15:O:376:TYR:HB2	15:O:419:LYS:HD3	1.79	0.63
16:P:438:TRP:HZ2	18:R:297:PHE:CE1	2.15	0.63
17:Q:193:PHE:CD2	18:R:208:TYR:CE2	2.85	0.63
1:A:476:VAL:HG13	2:B:1070:ARG:HA	1.81	0.63
2:B:527:PHE:CE2	2:B:666:PRO:CB	2.82	0.63
18:R:75:GLN:HA	18:R:78:ARG:HE	1.64	0.63
18:R:180:CYS:SG	18:R:185:LYS:HG2	2.39	0.63
1:A:1482:LYS:O	2:B:308:LEU:CD2	2.38	0.63
15:O:181:ARG:HH11	15:O:181:ARG:CG	2.12	0.63
16:P:368:HIS:HB3	16:P:411:LYS:HZ2	1.63	0.63
16:P:454:GLN:HA	16:P:455:LYS:HE2	1.79	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:50:ASN:OD1	2:B:167:SER:HB2	1.99	0.63
2:B:897:GLU:HA	12:L:46:VAL:CG2	2.29	0.63
1:A:83:VAL:HG13	1:A:427:PHE:CE2	2.34	0.63
6:F:69:LEU:O	6:F:143:PHE:CE2	2.52	0.63
7:G:158:LYS:HB3	15:O:105:ASN:OD1	1.99	0.63
15:O:376:TYR:CD1	15:O:419:LYS:HD3	2.34	0.63
1:A:472:MET:CG	2:B:1073:GLU:OE1	2.46	0.63
2:B:64:GLY:CA	2:B:242:ASP:CB	2.74	0.63
2:B:894:LYS:CG	12:L:47:ARG:NE	2.62	0.63
2:B:1072:GLY:O	2:B:1076:ARG:N	2.31	0.63
1:A:475:ARG:O	2:B:1059:PRO:HG2	1.99	0.63
1:A:581:ILE:HD11	1:A:585:ASP:HB3	1.81	0.63
1:A:921:PRO:HD2	8:H:19:ARG:CG	2.28	0.63
16:P:185:GLN:NE2	18:R:197:PRO:HB3	2.14	0.63
16:P:354:PRO:HG3	18:R:31:PHE:CG	2.34	0.63
16:P:532:GLU:HB2	16:P:554:ASN:HB3	1.81	0.63
17:Q:19:LEU:HD11	17:Q:27:ARG:CB	2.27	0.63
1:A:432:ASN:OD1	1:A:443:ALA:HA	1.99	0.62
1:A:472:MET:HB3	2:B:1073:GLU:CG	2.29	0.62
2:B:143:TRP:HB3	2:B:446:MET:CE	2.25	0.62
2:B:1096:SER:O	2:B:1097:ASP:CB	2.47	0.62
15:O:245:GLN:NE2	15:O:245:GLN:HA	2.14	0.62
16:P:675:PHE:HE2	16:P:741:ILE:HG21	1.63	0.62
17:Q:6:ARG:O	17:Q:7:GLY:O	2.17	0.62
1:A:1329:ILE:CB	1:A:1456:PHE:HE2	2.12	0.62
2:B:152:LEU:CB	2:B:443:LYS:CE	2.23	0.62
5:E:197:LYS:HD3	5:E:199:ILE:HD11	1.79	0.62
17:Q:10:CYS:CB	17:Q:17:SER:H	2.13	0.62
17:Q:356:VAL:CG1	18:R:208:TYR:CE1	2.73	0.62
1:A:1055:ILE:HD13	1:A:1178:LEU:HD23	1.80	0.62
2:B:1069:ILE:O	2:B:1070:ARG:CB	2.45	0.62
15:O:181:ARG:HB2	15:O:181:ARG:NH1	2.12	0.62
16:P:197:ARG:NE	16:P:261:VAL:HG22	2.14	0.62
16:P:434:ARG:CG	18:R:143:THR:HG21	2.23	0.62
16:P:665:ASN:OD1	16:P:665:ASN:N	2.31	0.62
18:R:202:THR:C	18:R:205:VAL:HG23	2.19	0.62
18:R:248:LYS:CB	18:R:298:GLN:NE2	2.61	0.62
1:A:436:ALA:CA	1:A:439:ASP:C	2.66	0.62
1:A:721:LYS:HZ3	8:H:90:ALA:C	2.00	0.62
1:A:1484:LEU:HD11	2:B:305:ARG:NE	2.14	0.62
2:B:29:PRO:O	2:B:178:TYR:N	2.29	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:143:TRP:CE3	2:B:446:MET:CE	2.82	0.62
6:F:72:LYS:CG	6:F:142:SER:CB	2.77	0.62
16:P:388:ASN:HB3	18:R:151:PRO:HB2	1.81	0.62
16:P:432:PRO:HB2	18:R:146:SER:HB2	1.81	0.62
17:Q:351:ASN:O	17:Q:369:TRP:HH2	1.82	0.62
18:R:308:PHE:HD1	18:R:309:ALA:H	1.46	0.62
1:A:1329:ILE:CB	1:A:1456:PHE:CE2	2.82	0.62
2:B:1072:GLY:O	2:B:1075:GLU:CB	2.47	0.62
6:F:66:ARG:HH21	7:G:90:LEU:HD13	1.64	0.62
16:P:436:ILE:HG12	18:R:141:TRP:CE3	2.34	0.62
18:R:202:THR:CA	18:R:205:VAL:CG2	2.75	0.62
1:A:486:PRO:HG2	2:B:781:TYR:CA	2.29	0.62
1:A:825:ALA:HB3	2:B:1022:LEU:HB3	1.82	0.62
1:A:826:PHE:CD1	2:B:777:SER:CB	2.83	0.62
2:B:697:LEU:CB	2:B:702:ASN:ND2	2.59	0.62
15:O:56:VAL:HG21	15:O:99:ILE:HD12	1.82	0.62
15:O:515:ASN:HD21	15:O:547:ASN:HD21	1.47	0.62
16:P:724:LEU:HD13	17:Q:447:ALA:HB2	1.81	0.62
1:A:493:ASN:CB	1:A:654:ASP:OD1	2.47	0.62
1:A:506:THR:HG21	1:A:578:TYR:O	1.98	0.62
1:A:729:LYS:HD2	8:H:120:GLY:HA3	1.82	0.62
1:A:799:GLU:HG3	1:A:1062:HIS:ND1	2.14	0.62
1:A:827:THR:CG2	1:A:924:SER:HB3	2.30	0.62
2:B:45:HIS:NE2	2:B:500:PHE:HB3	2.13	0.62
2:B:64:GLY:CA	2:B:242:ASP:HB3	2.28	0.62
15:O:100:LEU:HD22	15:O:107:ILE:HD11	1.82	0.62
15:O:361:PHE:O	15:O:365:THR:HG23	1.99	0.62
15:O:396:MET:HE1	15:O:433:LYS:C	2.20	0.62
1:A:1657:LEU:HB3	7:G:104:LEU:HD22	1.81	0.62
2:B:547:HIS:HB2	2:B:698:SER:HA	1.81	0.62
15:O:67:ASP:OD1	15:O:69:THR:HB	2.00	0.62
16:P:662:LEU:O	16:P:665:ASN:ND2	2.31	0.62
18:R:26:TYR:HB3	18:R:169:PRO:HB3	1.81	0.62
2:B:897:GLU:HA	12:L:46:VAL:HG23	1.80	0.62
15:O:450:LEU:O	15:O:454:VAL:HG12	1.99	0.62
16:P:189:THR:O	16:P:450:ARG:NH2	2.33	0.62
17:Q:212:VAL:O	17:Q:216:GLU:HG2	1.98	0.62
18:R:171:ARG:O	18:R:174:GLU:N	2.33	0.62
1:A:477:ASN:CA	2:B:1047:ARG:HD3	2.29	0.62
2:B:1090:ASP:O	2:B:1094:ASN:N	2.33	0.62
7:G:241:ARG:CZ	15:O:189:PHE:HB3	2.29	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:R:305:THR:HB	18:R:308:PHE:HE1	1.64	0.62
1:A:467:PHE:CD2	1:A:1614:SER:HB2	2.34	0.61
1:A:545:SER:N	17:Q:34:VAL:CB	2.63	0.61
1:A:1049:MET:HB2	1:A:1052:GLY:HA2	1.80	0.61
1:A:1318:SER:OG	1:A:1450:ILE:HD11	2.00	0.61
15:O:510:VAL:CG1	15:O:543:ILE:HD12	2.30	0.61
16:P:436:ILE:O	18:R:141:TRP:CG	2.53	0.61
16:P:473:HIS:CD2	16:P:475:ARG:HD2	2.35	0.61
17:Q:198:ILE:HG21	17:Q:388:THR:HG22	1.82	0.61
1:A:438:ILE:O	1:A:457:LYS:CG	2.48	0.61
1:A:1050:TYR:CE1	1:A:1185:VAL:HG11	2.35	0.61
2:B:184:LYS:HB3	2:B:735:HIS:CG	2.35	0.61
2:B:1091:ARG:O	2:B:1096:SER:HB2	2.01	0.61
3:C:272:LYS:HG3	14:N:175:TYR:HE1	1.65	0.61
6:F:70:LYS:HA	6:F:73:ALA:HB3	1.82	0.61
15:O:374:PRO:O	15:O:376:TYR:CB	2.39	0.61
16:P:365:TRP:HB2	16:P:371:LYS:O	2.00	0.61
16:P:775:TRP:O	17:Q:113:LYS:NZ	2.33	0.61
16:P:397:LYS:NZ	18:R:85:ARG:CG	2.62	0.61
1:A:1050:TYR:CE1	1:A:1179:ILE:CG1	2.76	0.61
1:A:1314:GLN:HE22	1:A:1446:ARG:CZ	2.12	0.61
2:B:1120:ILE:HD12	15:O:117:GLN:HE21	1.61	0.61
15:O:373:LEU:CD1	15:O:423:TYR:CD2	2.84	0.61
15:O:467:MET:CG	15:O:575:SER:HA	2.30	0.61
16:P:394:VAL:CG1	18:R:144:VAL:HB	2.30	0.61
16:P:422:ILE:O	16:P:439:LYS:HB2	2.01	0.61
17:Q:351:ASN:CA	17:Q:369:TRP:CZ2	2.84	0.61
1:A:422:ARG:CZ	18:R:412:ARG:NH1	2.63	0.61
1:A:878:ARG:HG3	9:I:66:VAL:CG2	2.27	0.61
15:O:200:ASN:ND2	17:Q:14:ASN:C	2.53	0.61
16:P:388:ASN:HB3	18:R:151:PRO:CB	2.29	0.61
16:P:389:TRP:CZ2	18:R:148:ASN:N	2.68	0.61
18:R:157:MET:HG3	18:R:162:PHE:HB2	1.81	0.61
1:A:966:LEU:HD22	1:A:997:PHE:CE1	2.36	0.61
2:B:848:ILE:CA	12:L:60:ARG:CD	2.72	0.61
7:G:141:SER:CB	15:O:142:ILE:HD11	2.20	0.61
15:O:581:THR:HA	15:O:584:GLN:NE2	2.15	0.61
16:P:383:ILE:HG12	16:P:390:GLN:HG2	1.81	0.61
17:Q:3:THR:HG22	17:Q:20:TRP:CB	2.29	0.61
1:A:475:ARG:C	2:B:1059:PRO:HG2	2.21	0.61
2:B:549:CYS:HG	2:B:649:MET:HG2	1.62	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:683:ASN:CA	14:N:154:ARG:HH22	2.14	0.61
16:P:362:ARG:HB3	16:P:375:PHE:HB2	1.82	0.61
16:P:717:LYS:NZ	20:P:903:SO4:O1	2.27	0.61
1:A:467:PHE:CD2	1:A:1614:SER:CB	2.84	0.61
1:A:1298:ASP:CA	1:A:1468:LYS:HZ3	2.14	0.61
2:B:146:ASN:ND2	2:B:441:LYS:HE3	2.15	0.61
3:C:272:LYS:HG3	14:N:175:TYR:CE1	2.36	0.61
16:P:625:ASP:O	16:P:629:ARG:HB3	2.00	0.61
17:Q:24:ASP:OD1	17:Q:26:ARG:NH1	2.31	0.61
17:Q:193:PHE:HD2	18:R:208:TYR:CD2	2.16	0.61
17:Q:503:SER:O	17:Q:507:ASN:ND2	2.33	0.61
1:A:990:ILE:CG1	1:A:994:GLU:C	2.69	0.61
2:B:202:LEU:HD23	2:B:202:LEU:N	2.11	0.61
2:B:203:ILE:HB	2:B:405:GLY:HA3	1.82	0.61
2:B:563:SER:HA	13:M:73:SER:CB	2.31	0.61
2:B:563:SER:HB3	13:M:73:SER:HB3	1.82	0.61
2:B:1079:LEU:HD22	2:B:1084:THR:OG1	2.00	0.61
15:O:376:TYR:CE1	15:O:588:LEU:HD22	2.25	0.61
1:A:966:LEU:CD2	1:A:997:PHE:HZ	2.11	0.61
2:B:796:ARG:O	10:J:8:PHE:HE1	1.83	0.61
6:F:74:ILE:HG21	6:F:144:GLU:HG2	1.81	0.61
16:P:348:HIS:NE2	18:R:154:LYS:CD	2.64	0.61
16:P:397:LYS:HZ1	18:R:85:ARG:CG	2.13	0.61
1:A:472:MET:SD	2:B:1073:GLU:CD	2.79	0.60
1:A:995:TYR:OH	2:B:715:ASN:CG	2.39	0.60
1:A:1226:VAL:HG12	1:A:1227:MET:HG2	1.83	0.60
1:A:1313:LEU:HD23	1:A:1462:PHE:CZ	2.29	0.60
1:A:1314:GLN:OE1	1:A:1446:ARG:CD	2.48	0.60
2:B:995:TYR:OH	14:N:163:VAL:HG23	2.01	0.60
16:P:197:ARG:HE	16:P:261:VAL:N	1.93	0.60
18:R:251:TRP:HE3	18:R:307:LYS:NZ	1.99	0.60
2:B:399:HIS:C	2:B:400:GLN:HG3	2.20	0.60
3:C:314:PHE:CD2	11:K:135:PHE:CZ	2.89	0.60
16:P:21:GLN:HB2	18:R:139:GLU:OE1	2.00	0.60
16:P:484:ARG:O	16:P:486:ALA:N	2.32	0.60
16:P:641:TRP:HZ2	16:P:656:HIS:HB3	1.67	0.60
1:A:1330:VAL:CG2	1:A:1455:ARG:HD2	2.31	0.60
2:B:143:TRP:HB2	2:B:446:MET:HE3	0.67	0.60
2:B:1072:GLY:C	2:B:1075:GLU:CG	2.51	0.60
8:H:25:ARG:NH1	8:H:27:GLU:OE2	2.34	0.60
15:O:201:LYS:CD	15:O:239:SER:OG	2.49	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:474:LYS:O	2:B:1070:ARG:HG3	2.01	0.60
16:P:197:ARG:HG3	16:P:261:VAL:O	2.01	0.60
17:Q:291:ASP:OD2	17:Q:291:ASP:N	2.32	0.60
1:A:670:ILE:HG12	2:B:783:MET:HE3	1.82	0.60
1:A:991:LYS:CB	1:A:993:GLN:OE1	2.44	0.60
1:A:1600:ARG:CG	1:A:1616:GLU:OE1	2.49	0.60
6:F:72:LYS:CA	6:F:142:SER:CB	2.59	0.60
15:O:582:ARG:O	15:O:586:ILE:HG13	2.02	0.60
1:A:413:LEU:O	1:A:416:ARG:CG	2.49	0.60
2:B:143:TRP:CG	2:B:446:MET:CE	2.65	0.60
17:Q:358:PRO:HA	18:R:206:ARG:CZ	2.26	0.60
1:A:1003:ARG:NH2	2:B:530:PRO:CA	2.65	0.60
1:A:1660:VAL:C	7:G:102:GLU:HG2	2.22	0.60
17:Q:10:CYS:HB2	17:Q:17:SER:H	1.67	0.60
1:A:438:ILE:O	1:A:457:LYS:HD3	1.96	0.60
2:B:205:MET:CE	2:B:500:PHE:O	2.47	0.60
2:B:345:SER:HA	13:M:113:ILE:HG12	1.83	0.60
2:B:923:GLN:NE2	2:B:957:ARG:HD2	2.16	0.60
2:B:1005:TYR:CZ	14:N:170:HIS:CE1	2.89	0.60
15:O:438:GLN:O	15:O:441:PHE:HB3	2.02	0.60
16:P:67:ASP:OD1	16:P:545:SER:OG	2.15	0.60
17:Q:382:GLU:HB2	18:R:241:ARG:NH1	2.17	0.60
18:R:250:LEU:HB2	18:R:270:PHE:CE2	2.37	0.60
1:A:399:LEU:HD21	1:A:423:LEU:CD2	2.30	0.60
2:B:228:SER:HB2	2:B:253:LEU:HD23	1.84	0.60
5:E:93:MET:HG3	5:E:120:ALA:HB1	1.82	0.60
7:G:242:VAL:HG21	15:O:183:ILE:CG2	2.32	0.60
15:O:376:TYR:CZ	15:O:588:LEU:CD2	2.76	0.60
16:P:319:ASP:HB2	16:P:363:ILE:HG12	1.83	0.60
1:A:613:THR:HG21	2:B:913:ILE:HG22	1.81	0.60
1:A:1329:ILE:HG22	1:A:1456:PHE:CE2	2.30	0.60
2:B:497:ILE:CG1	2:B:699:ILE:CD1	2.79	0.60
3:C:58:ASN:HA	3:C:296:ASN:HD21	0.78	0.60
15:O:348:THR:HG22	15:O:351:SER:CB	2.26	0.60
1:A:435:ASN:HB3	1:A:442:LYS:CA	2.32	0.59
1:A:953:GLU:HB3	1:A:1205:PHE:CE2	2.37	0.59
1:A:1606:SER:CB	1:A:1611:MET:CE	2.79	0.59
2:B:679:GLN:CA	14:N:155:VAL:O	2.50	0.59
15:O:370:THR:OG1	15:O:371:HIS:HD2	1.84	0.59
17:Q:9:ILE:HB	17:Q:16:PRO:CB	2.26	0.59
18:R:173:MET:CG	18:R:188:PHE:HZ	2.11	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:489:ASN:CB	11:K:95:HIS:CD2	2.85	0.59
2:B:143:TRP:CD2	2:B:446:MET:CE	2.85	0.59
2:B:143:TRP:CZ2	2:B:446:MET:CA	2.84	0.59
2:B:207:ILE:O	2:B:207:ILE:HG22	2.02	0.59
15:O:602:TYR:HD2	15:O:605:LEU:HD23	1.66	0.59
16:P:473:HIS:NE2	18:R:1:MET:SD	2.74	0.59
3:C:228:ARG:HD3	14:N:173:THR:OG1	2.02	0.59
13:M:101:VAL:HG12	13:M:105:SER:OG	2.01	0.59
1:A:83:VAL:HG11	1:A:427:PHE:CE2	2.37	0.59
1:A:415:ASP:HA	1:A:418:VAL:HG12	1.84	0.59
1:A:699:CYS:O	1:A:815:ARG:NH1	2.35	0.59
16:P:348:HIS:CG	18:R:154:LYS:HD3	2.34	0.59
1:A:246:ASP:HB3	1:A:248:PHE:H	1.66	0.59
1:A:629:ASP:HA	2:B:926:VAL:HG23	1.84	0.59
2:B:65:VAL:CG2	2:B:417:ILE:HD12	2.32	0.59
2:B:143:TRP:CH2	2:B:446:MET:HG3	2.37	0.59
3:C:45:SER:HB2	3:C:271:ARG:NH2	2.18	0.59
7:G:241:ARG:HG2	15:O:152:GLN:OE1	2.02	0.59
16:P:631:SER:O	16:P:686:TYR:OH	2.20	0.59
1:A:422:ARG:NH1	18:R:412:ARG:HH11	1.96	0.59
1:A:618:TYR:HE1	2:B:783:MET:HB2	1.67	0.59
1:A:862:THR:HG22	9:I:67:VAL:HG11	1.83	0.59
1:A:998:HIS:CD2	2:B:712:SER:H	2.20	0.59
2:B:200:GLU:OE2	2:B:736:ARG:NH2	2.34	0.59
2:B:743:ARG:CZ	10:J:60:PHE:CZ	2.83	0.59
3:C:322:LYS:NZ	11:K:129:ASP:OD1	2.35	0.59
17:Q:369:TRP:HB3	17:Q:373:GLU:OE2	2.02	0.59
1:A:878:ARG:HG2	9:I:67:VAL:CG1	2.05	0.59
7:G:24:VAL:HA	7:G:25:THR:CA	2.25	0.59
15:O:200:ASN:ND2	17:Q:14:ASN:CB	2.65	0.59
15:O:224:GLU:OE1	15:O:224:GLU:N	2.23	0.59
16:P:626:LEU:HD11	16:P:665:ASN:HB2	1.84	0.59
1:A:474:LYS:HE3	2:B:1092:LEU:HD21	1.77	0.59
2:B:110:ASN:O	2:B:112:GLY:N	2.35	0.59
6:F:74:ILE:C	7:G:95:LEU:CD1	2.62	0.59
1:A:953:GLU:CB	1:A:1205:PHE:CD2	2.86	0.59
1:A:1650:GLY:O	1:A:1653:SER:N	2.35	0.59
2:B:28:PRO:HD3	10:J:62:ARG:NE	2.17	0.59
2:B:143:TRP:NE1	2:B:446:MET:HB2	2.18	0.59
2:B:497:ILE:HG12	2:B:699:ILE:CD1	2.33	0.59
2:B:531:VAL:CG1	2:B:716:MET:HA	2.33	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:O:227:PHE:CD1	15:O:363:THR:HB	2.38	0.59
15:O:240:ILE:HG23	15:O:332:LEU:CD1	2.33	0.59
17:Q:418:PRO:CD	18:R:233:TYR:OH	2.50	0.59
1:A:414:GLU:O	1:A:417:ARG:N	2.33	0.59
1:A:1606:SER:HB2	1:A:1611:MET:CE	2.33	0.59
2:B:209:GLN:O	2:B:401:GLU:HG2	2.03	0.59
2:B:538:PRO:HB2	2:B:542:LEU:HG	1.84	0.59
5:E:55:ARG:NH2	5:E:113:GLN:OE1	2.36	0.59
15:O:375:THR:O	15:O:377:TYR:N	2.35	0.59
16:P:55:LEU:HD23	18:R:227:HIS:CG	2.37	0.59
17:Q:321:ASP:O	17:Q:324:ARG:N	2.27	0.59
18:R:206:ARG:HE	18:R:206:ARG:N	1.97	0.59
1:A:1260:LYS:HE2	1:A:1262:LEU:CD2	2.33	0.58
1:A:1608:SER:OG	1:A:1632:GLU:OE2	2.12	0.58
2:B:30:LYS:C	2:B:176:SER:CB	2.72	0.58
2:B:1069:ILE:H	2:B:1069:ILE:CD1	2.16	0.58
7:G:30:GLU:HA	7:G:32:ASN:N	2.18	0.58
8:H:80:ARG:HG3	11:K:108:TYR:OH	2.03	0.58
15:O:607:LYS:HG3	15:O:608:GLU:N	2.17	0.58
16:P:317:ILE:HG22	16:P:363:ILE:HD13	1.84	0.58
16:P:389:TRP:HZ2	18:R:147:GLN:CA	2.16	0.58
16:P:715:TYR:CE1	16:P:733:THR:HG23	2.38	0.58
17:Q:413:LEU:CG	18:R:273:TRP:CZ2	2.74	0.58
1:A:477:ASN:O	2:B:1047:ARG:CG	2.51	0.58
1:A:1003:ARG:NH2	2:B:530:PRO:HA	2.17	0.58
16:P:384:ASP:OD2	16:P:387:ASN:HB2	2.03	0.58
16:P:662:LEU:HB3	16:P:665:ASN:HD21	1.67	0.58
16:P:675:PHE:CZ	16:P:742:TRP:HZ3	2.21	0.58
16:P:719:LEU:HD13	16:P:733:THR:HG21	1.85	0.58
16:P:725:VAL:HG21	17:Q:446:TYR:CD1	2.38	0.58
17:Q:436:LEU:HD12	17:Q:436:LEU:H	1.67	0.58
18:R:250:LEU:HB2	18:R:270:PHE:HE2	1.67	0.58
1:A:408:LYS:HE3	1:A:416:ARG:NH1	2.19	0.58
1:A:995:TYR:CZ	2:B:707:SER:CB	2.72	0.58
1:A:1187:ILE:HG13	2:B:1080:ILE:HG22	1.85	0.58
2:B:75:ASP:CA	2:B:440:PHE:CZ	2.86	0.58
2:B:203:ILE:HG21	2:B:405:GLY:CA	2.33	0.58
2:B:829:ASN:OD1	2:B:829:ASN:N	2.36	0.58
12:L:38:LEU:HD12	12:L:49:LYS:HG3	1.85	0.58
16:P:479:HIS:NE2	16:P:491:SER:OG	2.24	0.58
16:P:484:ARG:HD2	16:P:488:LEU:HD12	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:R:199:LYS:HZ1	18:R:204:GLU:CA	2.13	0.58
18:R:350:SER:O	18:R:354:LEU:HB2	2.03	0.58
1:A:408:LYS:HE3	1:A:416:ARG:HH12	1.67	0.58
1:A:718:THR:CG2	8:H:118:PHE:HB3	2.34	0.58
1:A:1657:LEU:CD2	7:G:104:LEU:CD1	2.61	0.58
17:Q:222:PHE:HA	17:Q:492:ALA:HB1	1.86	0.58
17:Q:441:ASP:O	17:Q:445:ARG:HG2	2.02	0.58
18:R:317:LEU:HD13	18:R:367:ILE:HD13	1.85	0.58
1:A:470:HIS:HB3	2:B:1058:GLN:HE22	1.68	0.58
1:A:478:TYR:CB	2:B:1048:SER:O	2.50	0.58
1:A:581:ILE:HB	1:A:637:PHE:CE2	2.38	0.58
1:A:1050:TYR:CB	1:A:1054:ALA:HA	2.33	0.58
1:A:1330:VAL:HG22	1:A:1455:ARG:CD	2.34	0.58
15:O:510:VAL:HG12	15:O:543:ILE:HD12	1.86	0.58
16:P:436:ILE:CG2	18:R:143:THR:HA	2.34	0.58
17:Q:354:LYS:HD2	17:Q:369:TRP:HZ2	1.68	0.58
1:A:545:SER:N	17:Q:34:VAL:HB	2.19	0.58
1:A:828:CYS:SG	2:B:1027:TYR:CB	2.92	0.58
1:A:984:GLY:HA3	1:A:994:GLU:OE1	2.02	0.58
2:B:156:ARG:NH2	2:B:455:GLU:OE1	2.24	0.58
7:G:142:ALA:HB1	15:O:102:SER:O	2.03	0.58
16:P:473:HIS:C	16:P:504:THR:HG23	2.24	0.58
16:P:599:LYS:HE3	17:Q:272:GLN:HE22	1.69	0.58
16:P:659:LEU:HD12	16:P:742:TRP:CD1	2.39	0.58
17:Q:22:ILE:HD11	17:Q:26:ARG:HE	1.62	0.58
17:Q:162:ILE:HG21	17:Q:226:LEU:HD11	1.85	0.58
2:B:146:ASN:HD22	2:B:441:LYS:CE	2.15	0.58
6:F:72:LYS:NZ	6:F:140:ASP:OD2	2.21	0.58
14:N:69:SER:OG	14:N:70:LEU:N	2.37	0.58
15:O:219:ARG:NH2	15:O:360:VAL:CG2	2.67	0.58
17:Q:374:THR:CG2	18:R:219:LEU:HD13	2.34	0.58
1:A:408:LYS:HA	1:A:411:VAL:CG2	2.34	0.58
1:A:1204:THR:HG21	9:I:97:HIS:CB	2.33	0.58
2:B:923:GLN:HG2	2:B:949:ILE:HD11	1.85	0.58
14:N:89:ILE:HG12	14:N:139:VAL:HG22	1.85	0.58
16:P:489:PHE:CD2	18:R:138:PHE:CZ	2.92	0.58
17:Q:22:ILE:HD11	17:Q:26:ARG:CD	2.33	0.58
17:Q:369:TRP:CB	17:Q:373:GLU:OE2	2.51	0.58
1:A:4:SER:HB2	1:A:573:LEU:HD22	1.85	0.58
1:A:1074:TYR:HE2	1:A:1159:ASP:HB3	1.68	0.58
15:O:348:THR:HG23	15:O:351:SER:H	1.68	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:P:268:SER:OG	16:P:269:PHE:N	2.36	0.58
1:A:396:ILE:HD11	1:A:426:ALA:HB1	1.84	0.58
15:O:190:ILE:HA	15:O:193:TYR:CD2	2.39	0.58
15:O:376:TYR:CZ	15:O:419:LYS:HE2	2.38	0.58
16:P:274:ILE:O	16:P:289:SER:CB	2.44	0.58
16:P:436:ILE:CA	18:R:143:THR:HG23	2.34	0.58
2:B:683:ASN:HA	14:N:150:TYR:CE2	2.39	0.57
3:C:37:LYS:HG3	11:K:134:LYS:HZ2	1.69	0.57
11:K:49:LEU:HD23	11:K:51:THR:HG23	1.86	0.57
12:L:33:GLU:HG3	12:L:53:HIS:CE1	2.39	0.57
15:O:200:ASN:ND2	17:Q:14:ASN:OD1	2.36	0.57
16:P:348:HIS:CD2	18:R:154:LYS:CD	2.72	0.57
16:P:397:LYS:CG	18:R:85:ARG:HD3	2.34	0.57
17:Q:337:SER:HB2	17:Q:448:LYS:HD3	1.86	0.57
1:A:407:GLN:O	1:A:408:LYS:NZ	2.38	0.57
1:A:506:THR:HB	1:A:579:ARG:O	2.03	0.57
1:A:938:VAL:CG2	9:I:82:ILE:CD1	2.68	0.57
2:B:152:LEU:CG	2:B:443:LYS:HE3	2.27	0.57
2:B:679:GLN:HG3	14:N:156:PRO:N	2.18	0.57
2:B:796:ARG:NH2	10:J:8:PHE:O	2.37	0.57
16:P:438:TRP:HZ2	18:R:297:PHE:HE1	1.51	0.57
18:R:181:THR:O	18:R:185:LYS:HG3	2.04	0.57
1:A:615:ARG:HH12	2:B:929:ARG:CD	2.17	0.57
3:C:274:THR:CB	14:N:172:ALA:HB2	2.25	0.57
13:M:10:ILE:HB	14:N:70:LEU:HB3	1.86	0.57
16:P:186:TYR:CZ	18:R:196:GLU:OE1	2.57	0.57
16:P:420:GLU:HA	16:P:442:LEU:O	2.03	0.57
16:P:436:ILE:N	18:R:143:THR:N	2.51	0.57
17:Q:8:PRO:O	17:Q:9:ILE:C	2.42	0.57
17:Q:371:GLU:HG3	18:R:231:LEU:HD11	1.85	0.57
18:R:9:THR:HB	18:R:205:VAL:HG13	1.86	0.57
1:A:422:ARG:HH12	18:R:412:ARG:NH1	1.79	0.57
1:A:476:VAL:HG22	2:B:1069:ILE:N	2.18	0.57
11:K:68:GLU:HG2	11:K:72:LEU:HD23	1.86	0.57
15:O:379:ARG:HH11	15:O:379:ARG:CA	2.09	0.57
16:P:365:TRP:HB3	16:P:372:ILE:HG22	1.86	0.57
17:Q:12:THR:HB	17:Q:33:HIS:ND1	2.18	0.57
3:C:42:VAL:HB	11:K:138:LYS:HG3	1.86	0.57
3:C:293:ARG:N	3:C:295:ARG:CZ	2.55	0.57
15:O:219:ARG:CZ	15:O:360:VAL:HG22	2.34	0.57
16:P:317:ILE:HG13	16:P:326:ILE:HD13	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:P:357:LEU:CG	18:R:24:ILE:HD11	2.35	0.57
16:P:422:ILE:HG12	16:P:442:LEU:CD1	2.34	0.57
16:P:462:ILE:HB	16:P:483:HIS:HB3	1.87	0.57
17:Q:374:THR:HG23	18:R:219:LEU:CD1	2.35	0.57
1:A:991:LYS:N	1:A:994:GLU:CB	2.67	0.57
1:A:1032:VAL:HG21	1:A:1050:TYR:HE1	1.68	0.57
7:G:143:SER:OG	15:O:104:ILE:CG2	2.51	0.57
15:O:63:LEU:HD23	15:O:111:ARG:HD2	1.87	0.57
15:O:205:ARG:O	15:O:209:VAL:HG12	2.05	0.57
16:P:301:GLN:N	16:P:319:ASP:O	2.37	0.57
16:P:349:GLY:HA2	18:R:154:LYS:HA	1.85	0.57
17:Q:378:LEU:HD22	18:R:238:THR:OG1	2.04	0.57
1:A:672:ASP:OD1	2:B:777:SER:CB	2.53	0.57
2:B:833:PRO:HG2	2:B:836:TRP:CE2	2.40	0.57
16:P:382:GLU:OE1	18:R:146:SER:HB2	2.01	0.57
17:Q:22:ILE:HD12	17:Q:26:ARG:NE	2.18	0.57
2:B:49:PHE:CE2	2:B:194:PHE:CE2	2.93	0.57
1:A:1032:VAL:HG22	1:A:1050:TYR:CD1	2.39	0.57
1:A:1118:VAL:HG11	5:E:199:ILE:HG13	1.87	0.57
15:O:359:GLY:O	15:O:363:THR:CG2	2.53	0.57
16:P:407:ARG:HH22	16:P:411:LYS:HA	1.70	0.57
2:B:203:ILE:CG2	2:B:405:GLY:HA3	2.35	0.56
16:P:712:ASP:OD1	16:P:712:ASP:N	2.38	0.56
17:Q:356:VAL:CG1	18:R:208:TYR:HD1	2.09	0.56
1:A:986:PHE:CE2	2:B:958:MET:CE	2.88	0.56
1:A:1314:GLN:NE2	1:A:1446:ARG:NE	2.49	0.56
1:A:1484:LEU:HD11	2:B:305:ARG:CD	2.35	0.56
16:P:667:ASP:OD1	16:P:667:ASP:N	2.33	0.56
17:Q:193:PHE:CE2	18:R:208:TYR:CG	2.93	0.56
17:Q:362:THR:O	17:Q:365:ASP:HB2	2.04	0.56
17:Q:410:ARG:HE	17:Q:413:LEU:HD13	1.69	0.56
18:R:6:ILE:HD13	18:R:213:ILE:HB	1.83	0.56
1:A:472:MET:CG	2:B:1073:GLU:CD	2.73	0.56
1:A:474:LYS:CE	2:B:1092:LEU:HD22	2.33	0.56
1:A:615:ARG:CZ	2:B:929:ARG:HE	2.16	0.56
1:A:686:PHE:CZ	8:H:121:LEU:HD11	2.40	0.56
2:B:338:PHE:HZ	2:B:357:ILE:HD12	1.70	0.56
2:B:1013:MET:SD	2:B:1026:ILE:HG12	2.45	0.56
15:O:66:ASN:N	15:O:66:ASN:ND2	2.53	0.56
15:O:109:SER:OG	15:O:111:ARG:HG3	2.05	0.56
16:P:608:GLN:HA	16:P:611:ILE:HD12	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:Q:15:CYS:CB	17:Q:17:SER:N	2.59	0.56
17:Q:20:TRP:CE2	17:Q:28:THR:HB	2.39	0.56
17:Q:211:TYR:O	17:Q:214:ILE:HG22	2.05	0.56
18:R:180:CYS:SG	18:R:185:LYS:CG	2.94	0.56
1:A:475:ARG:HH22	2:B:1061:LYS:HG3	1.67	0.56
1:A:581:ILE:HG12	1:A:582:LYS:N	2.21	0.56
1:A:615:ARG:HH12	2:B:929:ARG:NE	2.02	0.56
16:P:358:SER:HB3	16:P:377:ARG:HD3	1.87	0.56
16:P:362:ARG:HH22	16:P:364:GLU:HG3	1.71	0.56
17:Q:417:PHE:CE2	18:R:270:PHE:CE1	2.75	0.56
1:A:408:LYS:H	1:A:408:LYS:HD3	1.70	0.56
1:A:535:GLN:HE22	17:Q:26:ARG:CG	2.17	0.56
1:A:615:ARG:HH12	2:B:929:ARG:HD3	1.71	0.56
1:A:721:LYS:NZ	8:H:91:ASP:CA	2.68	0.56
1:A:909:SER:HA	9:I:83:LYS:HE3	1.84	0.56
1:A:1310:LYS:CG	1:A:1311:GLU:OE1	2.37	0.56
2:B:184:LYS:CD	2:B:735:HIS:CD2	2.89	0.56
2:B:1005:TYR:CE1	14:N:170:HIS:CE1	2.93	0.56
5:E:159:ASP:OD1	5:E:162:ARG:NH1	2.38	0.56
7:G:143:SER:OG	15:O:104:ILE:HG22	2.01	0.56
15:O:243:GLU:HB3	15:O:332:LEU:CD1	2.30	0.56
1:A:670:ILE:HG13	2:B:783:MET:HE2	1.88	0.56
1:A:921:PRO:HD3	8:H:19:ARG:CG	2.33	0.56
1:A:1606:SER:CB	1:A:1611:MET:HE3	2.36	0.56
5:E:145:THR:O	5:E:147:HIS:N	2.38	0.56
13:M:15:VAL:HG22	13:M:90:LEU:HB2	1.88	0.56
15:O:234:ILE:CG1	15:O:367:LEU:HD13	2.36	0.56
16:P:375:PHE:HD1	16:P:402:ILE:HD13	1.69	0.56
17:Q:152:LEU:HB3	17:Q:154:LEU:HD22	1.85	0.56
17:Q:274:ILE:HG23	17:Q:282:ARG:HH22	1.71	0.56
18:R:5:PRO:HD3	18:R:217:THR:CB	2.23	0.56
1:A:1235:THR:O	1:A:1544:ASN:ND2	2.38	0.56
2:B:563:SER:HA	13:M:73:SER:OG	2.06	0.56
2:B:567:SER:O	14:N:140:SER:CB	2.52	0.56
16:P:198:ASP:CG	16:P:205:TYR:O	2.44	0.56
16:P:436:ILE:C	18:R:141:TRP:O	2.44	0.56
2:B:681:ILE:HB	14:N:154:ARG:CB	2.34	0.56
16:P:472:ARG:NE	18:R:200:THR:HG21	2.18	0.56
18:R:236:PHE:O	18:R:240:ILE:HG22	2.05	0.56
18:R:369:ALA:HB1	18:R:411:VAL:HG23	1.86	0.56
1:A:438:ILE:O	1:A:457:LYS:HB3	2.04	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1657:LEU:CB	7:G:104:LEU:HD13	2.35	0.56
2:B:30:LYS:HG2	2:B:178:TYR:CB	2.35	0.56
2:B:30:LYS:O	2:B:176:SER:CB	2.54	0.56
6:F:66:ARG:HH22	7:G:90:LEU:CB	2.19	0.56
6:F:70:LYS:CD	7:G:95:LEU:CD2	2.79	0.56
15:O:243:GLU:CB	15:O:332:LEU:CD1	2.84	0.56
15:O:375:THR:C	15:O:377:TYR:H	2.03	0.56
15:O:602:TYR:CD2	15:O:605:LEU:HD23	2.40	0.56
16:P:504:THR:HG22	16:P:505:PRO:HD2	1.88	0.56
18:R:4:VAL:CG2	18:R:214:VAL:CG1	2.79	0.56
18:R:83:HIS:O	18:R:85:ARG:N	2.39	0.56
1:A:1162:ASN:HD22	1:A:1165:LYS:HG3	1.71	0.56
1:A:1187:ILE:HG13	2:B:1080:ILE:CG2	2.36	0.56
2:B:864:ASP:CB	17:Q:412:LYS:CE	2.81	0.56
15:O:191:ASP:O	15:O:194:LEU:HB2	2.06	0.56
16:P:187:ILE:HB	16:P:188:GLN:CD	2.26	0.56
16:P:488:LEU:HB2	18:R:137:SER:OG	2.07	0.56
16:P:623:LEU:HG	16:P:678:LEU:HD12	1.88	0.56
17:Q:22:ILE:HD12	17:Q:24:ASP:OD1	2.04	0.56
18:R:173:MET:CG	18:R:188:PHE:CZ	2.87	0.56
1:A:502:ALA:HB1	1:A:530:TRP:NE1	2.21	0.55
3:C:86:PHE:HE2	3:C:205:LYS:HG3	1.69	0.55
10:J:10:CYS:HB3	10:J:43:ARG:NH1	2.21	0.55
13:M:11:GLU:N	13:M:86:LYS:O	2.36	0.55
17:Q:163:SER:HA	17:Q:230:ILE:HG22	1.88	0.55
18:R:4:VAL:CG2	18:R:214:VAL:CG2	2.65	0.55
1:A:797:LEU:HD13	1:A:809:VAL:HG21	1.87	0.55
1:A:998:HIS:NE2	2:B:711:GLN:HA	2.22	0.55
1:A:1499:ARG:O	1:A:1500:GLN:HB2	2.05	0.55
2:B:208:VAL:HG23	2:B:401:GLU:CG	2.35	0.55
8:H:80:ARG:NH1	11:K:108:TYR:CD1	2.74	0.55
16:P:436:ILE:HG22	18:R:142:ARG:CA	2.23	0.55
17:Q:411:ARG:O	17:Q:415:LYS:HB2	2.05	0.55
18:R:308:PHE:HD1	18:R:309:ALA:N	2.04	0.55
1:A:721:LYS:HE2	8:H:93:TYR:O	2.06	0.55
1:A:756:LYS:HD3	9:I:85:LYS:HZ3	1.30	0.55
1:A:756:LYS:HG3	9:I:85:LYS:HZ2	1.71	0.55
1:A:821:ILE:O	1:A:825:ALA:N	2.40	0.55
1:A:1658:ALA:HA	6:F:132:LEU:HA	1.87	0.55
3:C:314:PHE:CE2	11:K:135:PHE:CE1	2.95	0.55
7:G:56:ASN:HB3	7:G:59:GLN:HB3	1.87	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:P:474:LYS:O	16:P:499:GLU:HB2	2.07	0.55
17:Q:103:LEU:HD21	17:Q:205:ILE:HG21	1.88	0.55
17:Q:227:TYR:O	17:Q:230:ILE:HG13	2.06	0.55
17:Q:287:TRP:NE1	17:Q:289:ARG:HB3	2.21	0.55
17:Q:416:ILE:CD1	18:R:273:TRP:CD1	2.90	0.55
17:Q:8:PRO:HB2	17:Q:19:LEU:CD2	2.36	0.55
2:B:985:ILE:CG1	14:N:160:VAL:HG21	2.37	0.55
5:E:145:THR:C	5:E:147:HIS:H	2.10	0.55
15:O:376:TYR:CD2	15:O:419:LYS:HE2	2.40	0.55
16:P:473:HIS:ND1	16:P:473:HIS:O	2.37	0.55
18:R:246:GLN:HG2	18:R:247:ILE:H	1.71	0.55
1:A:476:VAL:HA	2:B:1059:PRO:HG2	1.88	0.55
2:B:1047:ARG:HG2	2:B:1049:THR:N	2.21	0.55
3:C:292:GLY:HA3	3:C:295:ARG:HH22	1.71	0.55
5:E:90:VAL:HG13	5:E:120:ALA:HA	1.88	0.55
16:P:426:ALA:C	16:P:433:VAL:HG11	2.27	0.55
16:P:534:VAL:HA	16:P:552:LEU:O	2.06	0.55
1:A:508:PRO:CD	1:A:639:GLN:HG3	2.37	0.55
7:G:144:HIS:CE1	15:O:145:SER:HB3	2.38	0.55
15:O:219:ARG:NE	15:O:230:TRP:HE1	2.05	0.55
15:O:332:LEU:CD2	15:O:599:LEU:HD21	2.36	0.55
15:O:578:SER:O	15:O:579:LEU:HB2	2.06	0.55
16:P:435:ARG:HH21	18:R:140:ILE:CD1	2.19	0.55
18:R:158:THR:HG23	18:R:161:ASN:H	1.72	0.55
18:R:187:TYR:O	18:R:191:ILE:HG23	2.07	0.55
18:R:353:VAL:CG1	18:R:364:VAL:HB	2.36	0.55
1:A:436:ALA:CA	1:A:440:SER:HA	2.37	0.55
1:A:953:GLU:HB3	1:A:1205:PHE:CZ	2.41	0.55
1:A:1260:LYS:HE2	1:A:1262:LEU:HG	1.89	0.55
1:A:1484:LEU:CD1	2:B:305:ARG:NH1	2.56	0.55
1:A:1650:GLY:O	1:A:1651:THR:C	2.41	0.55
2:B:322:ASN:HB3	2:B:325:GLN:H	1.71	0.55
3:C:139:LYS:HG2	3:C:201:GLU:HB3	1.89	0.55
15:O:169:THR:HA	15:O:172:HIS:ND1	2.22	0.55
16:P:218:VAL:HG22	16:P:246:LYS:HB3	1.89	0.55
16:P:444:PRO:HG2	16:P:449:LEU:HD11	1.89	0.55
17:Q:113:LYS:HG3	17:Q:134:LYS:HZ1	1.71	0.55
1:A:697:TYR:CE2	11:K:92:SER:OG	2.58	0.55
1:A:966:LEU:HD22	1:A:997:PHE:CZ	2.40	0.55
1:A:990:ILE:CA	1:A:994:GLU:CB	2.64	0.55
2:B:203:ILE:CG2	2:B:405:GLY:HA2	2.37	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:236:ILE:HD13	2:B:377:MET:HE1	1.89	0.55
3:C:223:SER:HB3	10:J:12:LYS:HB2	1.87	0.55
3:C:315:PHE:CE2	11:K:139:ILE:CD1	2.89	0.55
15:O:69:THR:O	15:O:73:ILE:HG13	2.07	0.55
15:O:200:ASN:ND2	17:Q:14:ASN:CG	2.60	0.55
16:P:233:VAL:HG12	16:P:234:THR:H	1.71	0.55
17:Q:6:ARG:HA	17:Q:18:ARG:HD2	1.88	0.55
17:Q:290:THR:HB	17:Q:292:GLU:N	2.22	0.55
18:R:317:LEU:HD12	18:R:367:ILE:HD12	1.85	0.55
1:A:916:THR:O	1:A:919:LYS:NZ	2.40	0.55
2:B:401:GLU:HG3	2:B:402:VAL:H	1.70	0.55
15:O:163:ILE:HD12	15:O:207:LYS:HE3	1.89	0.55
15:O:376:TYR:HE2	15:O:377:TYR:HE2	1.44	0.55
16:P:434:ARG:CG	18:R:143:THR:HB	2.37	0.55
17:Q:193:PHE:HE2	18:R:208:TYR:CE2	2.25	0.55
18:R:320:CYS:O	18:R:323:SER:N	2.40	0.55
1:A:503:VAL:HG23	1:A:530:TRP:CB	2.19	0.54
1:A:827:THR:HG21	1:A:924:SER:HB3	1.89	0.54
2:B:54:GLU:HG3	2:B:168:ASN:HD21	1.71	0.54
2:B:625:GLU:OE1	2:B:667:PHE:HB3	2.07	0.54
2:B:1090:ASP:HA	2:B:1094:ASN:CG	2.27	0.54
3:C:315:PHE:HE2	11:K:139:ILE:HD12	1.70	0.54
15:O:359:GLY:O	15:O:363:THR:HG22	2.08	0.54
15:O:467:MET:HG2	15:O:575:SER:HA	1.89	0.54
18:R:26:TYR:CB	18:R:169:PRO:HB3	2.37	0.54
1:A:472:MET:CE	1:A:472:MET:CA	2.86	0.54
1:A:1276:THR:HG1	9:I:45:LEU:CD1	1.94	0.54
1:A:1606:SER:CB	1:A:1611:MET:HE2	2.37	0.54
2:B:48:SER:HB3	2:B:404:LEU:HD13	1.88	0.54
2:B:119:ARG:CZ	12:L:53:HIS:HE1	2.17	0.54
2:B:548:LYS:O	2:B:550:ARG:CZ	2.56	0.54
2:B:788:ILE:HB	2:B:948:ILE:HB	1.89	0.54
7:G:144:HIS:CE1	15:O:146:SER:OG	2.60	0.54
16:P:194:ARG:HA	16:P:209:LYS:O	2.06	0.54
16:P:315:PHE:HB3	16:P:317:ILE:CD1	2.37	0.54
16:P:389:TRP:CE3	18:R:149:LYS:O	2.60	0.54
16:P:448:THR:HG23	16:P:471:MET:H	1.71	0.54
1:A:403:LEU:HD11	1:A:419:ILE:HD13	1.88	0.54
1:A:1298:ASP:HA	1:A:1468:LYS:NZ	2.20	0.54
1:A:1641:ILE:HG23	2:B:1092:LEU:HD13	1.88	0.54
2:B:21:ARG:NH1	2:B:22:GLU:OE1	2.40	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:212:ASN:HD21	2:B:361:HIS:CB	2.20	0.54
3:C:33:VAL:CG1	11:K:130:VAL:HG21	2.38	0.54
16:P:352:PHE:CE1	18:R:157:MET:HG2	2.42	0.54
16:P:468:VAL:HG22	16:P:477:TYR:HB3	1.89	0.54
16:P:592:LEU:O	16:P:596:ILE:HG22	2.06	0.54
17:Q:318:LEU:HB3	17:Q:476:ILE:HD12	1.88	0.54
18:R:161:ASN:O	18:R:164:LYS:HB2	2.07	0.54
2:B:1073:GLU:HA	2:B:1076:ARG:CB	2.38	0.54
7:G:229:LEU:HD12	7:G:230:ARG:H	1.72	0.54
17:Q:196:SER:CB	17:Q:204:ARG:HG2	2.37	0.54
1:A:1162:ASN:HD21	1:A:1164:LYS:HB2	1.71	0.54
1:A:1655:ASP:N	6:F:135:ARG:O	2.36	0.54
2:B:64:GLY:CA	2:B:242:ASP:HB2	2.38	0.54
2:B:550:ARG:O	2:B:648:ARG:O	2.26	0.54
2:B:550:ARG:N	2:B:650:LEU:O	2.40	0.54
15:O:412:GLU:OE1	15:O:416:LYS:HD3	2.06	0.54
16:P:492:LEU:HD22	16:P:492:LEU:H	1.73	0.54
16:P:722:TRP:CD1	17:Q:264:PRO:HD3	2.42	0.54
1:A:67:LEU:HD13	1:A:71:PHE:O	2.08	0.54
1:A:589:MET:HE1	1:A:614:LEU:HD13	1.88	0.54
1:A:671:GLN:CB	2:B:952:HIS:CD2	2.90	0.54
2:B:212:ASN:OD1	2:B:238:SER:HA	2.08	0.54
2:B:679:GLN:N	14:N:155:VAL:O	2.41	0.54
2:B:894:LYS:HG2	12:L:47:ARG:CD	2.38	0.54
6:F:72:LYS:HB3	6:F:142:SER:HA	0.59	0.54
15:O:373:LEU:HD12	15:O:423:TYR:CD2	2.43	0.54
15:O:376:TYR:CE2	15:O:377:TYR:CD2	2.93	0.54
17:Q:335:THR:HG21	17:Q:478:ARG:HG3	1.89	0.54
1:A:408:LYS:HB2	1:A:411:VAL:O	2.08	0.54
1:A:449:GLY:O	1:A:451:VAL:N	2.34	0.54
1:A:909:SER:CA	9:I:83:LYS:NZ	2.61	0.54
2:B:203:ILE:HG22	2:B:405:GLY:HA2	1.90	0.54
2:B:373:MET:O	2:B:377:MET:HG3	2.07	0.54
14:N:87:TYR:HA	14:N:141:GLU:C	2.27	0.54
18:R:4:VAL:CB	18:R:214:VAL:HG22	2.38	0.54
1:A:1298:ASP:CG	1:A:1468:LYS:HZ3	2.11	0.54
2:B:284:SER:OG	2:B:287:GLU:HG3	2.07	0.54
2:B:317:TYR:HB3	2:B:320:LEU:HD12	1.89	0.54
3:C:315:PHE:CZ	11:K:139:ILE:HD12	2.42	0.54
11:K:48:LYS:HE2	11:K:64:GLN:NE2	2.23	0.54
16:P:221:ARG:HH12	16:P:266:GLU:HB3	1.72	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:P:659:LEU:HD12	16:P:742:TRP:NE1	2.23	0.54
16:P:711:LEU:HD21	16:P:741:ILE:HD13	1.90	0.54
17:Q:101:LYS:O	17:Q:105:LEU:HG	2.07	0.54
1:A:475:ARG:HD2	2:B:1059:PRO:O	2.07	0.54
1:A:492:THR:HG23	1:A:811:SER:OG	2.08	0.54
1:A:1262:LEU:HD23	1:A:1497:ILE:HA	1.90	0.54
2:B:679:GLN:OE1	14:N:157:ARG:HB2	2.06	0.54
2:B:1091:ARG:CZ	2:B:1095:SER:OG	2.56	0.54
3:C:97:LEU:HD11	3:C:202:ILE:HD13	1.90	0.54
16:P:436:ILE:CB	18:R:143:THR:CA	2.85	0.54
17:Q:162:ILE:HG22	17:Q:226:LEU:HD21	1.90	0.54
17:Q:505:ILE:HA	17:Q:508:ALA:HB3	1.90	0.54
1:A:719:ILE:HA	8:H:97:MET:HA	1.89	0.54
1:A:1297:PHE:CD2	9:I:60:LEU:HD13	2.43	0.54
1:A:1446:ARG:O	1:A:1450:ILE:HG13	2.08	0.54
1:A:1487:ASN:CG	2:B:305:ARG:HH22	2.11	0.54
1:A:1606:SER:HB2	1:A:1611:MET:HE2	1.89	0.54
2:B:699:ILE:O	2:B:703:LEU:HG	2.08	0.54
3:C:65:ASN:O	3:C:69:ARG:HG3	2.07	0.54
3:C:67:PHE:O	3:C:71:MET:HG3	2.08	0.54
7:G:132:VAL:HG22	7:G:232:THR:HG22	1.90	0.54
1:A:1322:ILE:C	1:A:1454:HIS:CD2	2.82	0.53
2:B:42:VAL:HG21	2:B:190:ILE:HD12	1.89	0.53
2:B:894:LYS:CA	12:L:54:ARG:HE	2.18	0.53
2:B:943:ILE:CD1	10:J:44:TYR:CZ	2.68	0.53
7:G:159:LYS:CD	15:O:103:ASN:CG	2.63	0.53
15:O:63:LEU:CD2	15:O:111:ARG:HD2	2.38	0.53
15:O:189:PHE:CD1	15:O:190:ILE:N	2.76	0.53
1:A:436:ALA:C	1:A:439:ASP:CA	2.76	0.53
1:A:472:MET:HE2	2:B:1076:ARG:CD	2.37	0.53
1:A:721:LYS:NZ	8:H:90:ALA:C	2.60	0.53
2:B:574:SER:O	13:M:97:VAL:HG22	2.07	0.53
2:B:859:CYS:HB3	2:B:872:LYS:HB2	1.88	0.53
15:O:235:GLU:O	15:O:238:ILE:HD13	2.08	0.53
15:O:240:ILE:HD13	15:O:240:ILE:N	2.23	0.53
16:P:184:SER:HA	18:R:198:LEU:CB	2.29	0.53
18:R:213:ILE:HG12	18:R:242:ILE:HD13	1.90	0.53
18:R:305:THR:HB	18:R:308:PHE:CE1	2.43	0.53
1:A:1136:VAL:HG22	1:A:1174:TYR:CG	2.44	0.53
1:A:1310:LYS:HG2	1:A:1311:GLU:CG	2.38	0.53
1:A:1654:PHE:CD2	6:F:134:ILE:HG23	2.44	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:O:100:LEU:HD22	15:O:107:ILE:CD1	2.38	0.53
16:P:184:SER:N	18:R:198:LEU:HD23	1.95	0.53
16:P:197:ARG:HB3	16:P:261:VAL:O	2.08	0.53
17:Q:361:PRO:O	17:Q:364:SER:N	2.42	0.53
18:R:168:ILE:HD11	18:R:172:LYS:HE2	1.90	0.53
18:R:350:SER:HA	18:R:353:VAL:HB	1.90	0.53
2:B:551:ILE:HG21	2:B:647:SER:CA	2.18	0.53
7:G:20:HIS:O	7:G:20:HIS:ND1	2.38	0.53
17:Q:341:ARG:NH2	17:Q:369:TRP:HE1	2.05	0.53
17:Q:385:PHE:CE1	18:R:209:ARG:HG3	2.44	0.53
2:B:16:PHE:HD2	10:J:32:GLU:OE2	1.90	0.53
2:B:38:LEU:HD11	2:B:493:PHE:CZ	2.43	0.53
2:B:38:LEU:HD11	2:B:493:PHE:HZ	1.74	0.53
3:C:230:LEU:HD22	3:C:297:HIS:CE1	2.43	0.53
16:P:273:ARG:HG2	16:P:291:PRO:HB3	1.90	0.53
17:Q:333:SER:HA	17:Q:336:GLU:HG2	1.89	0.53
1:A:824:THR:O	2:B:1023:ARG:HB2	2.08	0.53
1:A:1317:ILE:HA	1:A:1321:PHE:HB3	1.90	0.53
2:B:1005:TYR:HH	10:J:44:TYR:HE2	1.46	0.53
13:M:12:ILE:HD12	14:N:67:LEU:HB2	1.90	0.53
16:P:320:ILE:HG13	16:P:323:ASN:OD1	2.07	0.53
16:P:394:VAL:HG22	16:P:434:ARG:HH11	1.73	0.53
18:R:410:TYR:O	18:R:413:THR:OG1	2.20	0.53
1:A:1002:GLY:HA3	2:B:713:PRO:HD3	1.91	0.53
1:A:1298:ASP:O	1:A:1299:ASN:C	2.46	0.53
2:B:894:LYS:HG2	12:L:54:ARG:CZ	2.38	0.53
3:C:33:VAL:HG12	11:K:130:VAL:HG21	1.90	0.53
16:P:472:ARG:HH12	18:R:203:SER:HB2	1.74	0.53
17:Q:8:PRO:CB	17:Q:19:LEU:HD23	2.39	0.53
18:R:273:TRP:O	18:R:277:ILE:HG22	2.08	0.53
1:A:1298:ASP:CG	1:A:1468:LYS:HZ1	2.04	0.53
9:I:96:TYR:HA	9:I:111:PHE:O	2.09	0.53
13:M:75:GLN:HB2	14:N:60:SER:HA	1.91	0.53
15:O:206:ARG:HA	15:O:209:VAL:HG12	1.91	0.53
15:O:473:PHE:HE2	15:O:516:PRO:HG3	1.73	0.53
16:P:185:GLN:CB	18:R:195:LEU:CB	2.79	0.53
16:P:265:THR:HG23	16:P:274:ILE:HG12	1.90	0.53
1:A:481:ARG:HB3	2:B:1045:GLN:O	2.09	0.53
2:B:25:PHE:O	10:J:62:ARG:HD3	2.08	0.53
6:F:66:ARG:HH22	7:G:90:LEU:HD12	1.57	0.53
16:P:292:LEU:CD1	16:P:343:LEU:HG	2.39	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:P:436:ILE:HB	18:R:143:THR:CB	2.38	0.53
16:P:443:ASP:CB	18:R:3:GLU:OE2	2.52	0.53
17:Q:370:SER:O	17:Q:373:GLU:N	2.42	0.53
18:R:199:LYS:NZ	18:R:204:GLU:HB3	2.23	0.53
1:A:672:ASP:CG	2:B:777:SER:CB	2.77	0.53
1:A:1025:LYS:NZ	2:B:1076:ARG:NH1	2.56	0.53
15:O:243:GLU:HA	15:O:328:LEU:HD23	1.90	0.53
15:O:552:LEU:O	15:O:553:ARG:C	2.46	0.53
18:R:352:TRP:O	18:R:356:PRO:HD3	2.08	0.53
1:A:954:GLY:N	1:A:1205:PHE:HB3	2.10	0.52
1:A:1297:PHE:CZ	1:A:1301:GLU:OE1	2.52	0.52
2:B:497:ILE:CG1	2:B:699:ILE:HD13	2.38	0.52
2:B:679:GLN:HA	14:N:155:VAL:O	2.09	0.52
2:B:1005:TYR:CD2	14:N:170:HIS:CG	2.98	0.52
2:B:1065:ARG:O	2:B:1065:ARG:HG3	2.08	0.52
15:O:245:GLN:HG3	15:O:377:TYR:O	2.09	0.52
15:O:499:GLU:O	15:O:502:LEU:HG	2.09	0.52
16:P:436:ILE:CG2	18:R:143:THR:CA	2.87	0.52
17:Q:351:ASN:ND2	17:Q:373:GLU:OE1	2.41	0.52
18:R:252:GLY:O	18:R:256:GLU:CB	2.56	0.52
1:A:209:THR:HG21	5:E:173:SER:OG	2.09	0.52
1:A:544:VAL:HA	17:Q:34:VAL:H	1.74	0.52
2:B:134:ARG:HD2	2:B:160:GLY:HA3	1.91	0.52
2:B:894:LYS:HG2	12:L:47:ARG:HD2	1.90	0.52
15:O:376:TYR:CG	15:O:419:LYS:HD3	2.44	0.52
16:P:365:TRP:HE3	16:P:372:ILE:HG22	1.73	0.52
16:P:408:ILE:HB	16:P:453:VAL:HG21	1.91	0.52
16:P:448:THR:HG21	16:P:471:MET:H	1.74	0.52
18:R:347:ASP:O	18:R:351:GLU:CB	2.56	0.52
1:A:472:MET:CE	2:B:1076:ARG:CD	2.88	0.52
1:A:822:THR:O	2:B:1015:SER:HB2	2.09	0.52
1:A:862:THR:CA	9:I:67:VAL:HG12	2.39	0.52
16:P:302:VAL:O	16:P:363:ILE:HD11	2.09	0.52
18:R:242:ILE:HG23	18:R:244:GLY:H	1.74	0.52
2:B:404:LEU:O	2:B:405:GLY:C	2.47	0.52
2:B:548:LYS:O	2:B:549:CYS:C	2.47	0.52
15:O:337:THR:O	15:O:341:THR:OG1	2.27	0.52
17:Q:22:ILE:HD12	17:Q:26:ARG:NH1	2.24	0.52
1:A:382:GLN:NE2	1:A:456:VAL:HG22	2.23	0.52
1:A:403:LEU:CD1	1:A:419:ILE:HG23	2.35	0.52
2:B:833:PRO:O	2:B:834:LYS:HB3	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:272:LYS:HA	14:N:175:TYR:CD2	2.43	0.52
7:G:30:GLU:HA	7:G:32:ASN:H	1.74	0.52
7:G:35:SER:HG	7:G:132:VAL:H	1.57	0.52
15:O:402:THR:O	15:O:406:ILE:HG13	2.09	0.52
16:P:432:PRO:C	18:R:145:SER:OG	2.47	0.52
16:P:472:ARG:NH2	18:R:200:THR:HG23	2.21	0.52
1:A:1050:TYR:CD1	1:A:1179:ILE:CG2	2.85	0.52
15:O:467:MET:HG3	15:O:519:PHE:CZ	2.45	0.52
16:P:350:THR:CG2	18:R:153:ASN:OD1	2.58	0.52
16:P:436:ILE:HG12	18:R:141:TRP:CZ3	2.45	0.52
16:P:650:LEU:HD13	16:P:652:GLY:H	1.74	0.52
18:R:6:ILE:CD1	18:R:213:ILE:HG21	2.37	0.52
1:A:477:ASN:CA	2:B:1047:ARG:NH1	2.69	0.52
1:A:999:CYS:CA	2:B:712:SER:HB2	2.21	0.52
1:A:1654:PHE:CZ	6:F:89:GLU:HA	2.45	0.52
2:B:796:ARG:HB3	10:J:8:PHE:HD1	1.75	0.52
2:B:985:ILE:O	14:N:160:VAL:CG2	2.38	0.52
2:B:1092:LEU:CA	2:B:1096:SER:CB	2.79	0.52
15:O:200:ASN:OD1	17:Q:14:ASN:CG	2.47	0.52
15:O:518:LYS:HD3	15:O:519:PHE:CZ	2.45	0.52
1:A:497:VAL:HG21	1:A:605:VAL:HG13	1.92	0.52
1:A:613:THR:CG2	2:B:913:ILE:CG2	2.79	0.52
1:A:878:ARG:NH2	9:I:66:VAL:O	2.37	0.52
2:B:307:GLU:OE2	2:B:311:ARG:NH1	2.43	0.52
2:B:678:PRO:O	14:N:154:ARG:HA	2.10	0.52
3:C:45:SER:CB	3:C:271:ARG:NH2	2.71	0.52
4:D:80:THR:OG1	15:O:228:GLN:HG2	2.10	0.52
5:E:131:THR:HG21	5:E:191:LYS:HE2	1.91	0.52
15:O:248:LEU:HD23	15:O:248:LEU:O	2.10	0.52
16:P:436:ILE:HG22	18:R:143:THR:CA	2.38	0.52
16:P:573:GLU:HB2	17:Q:499:LYS:HZ3	1.75	0.52
1:A:1289:SER:HB3	1:A:1475:GLU:HG2	1.91	0.52
2:B:527:PHE:CG	2:B:666:PRO:HB3	2.44	0.52
17:Q:116:ILE:O	17:Q:120:ILE:HG12	2.09	0.52
17:Q:414:TYR:CD1	18:R:240:ILE:HG13	2.45	0.52
18:R:171:ARG:O	18:R:174:GLU:HB3	2.09	0.52
1:A:969:PHE:CE2	1:A:978:ALA:HA	2.44	0.52
1:A:1318:SER:HA	1:A:1450:ILE:CD1	2.39	0.52
2:B:22:GLU:O	2:B:26:ILE:HG13	2.10	0.52
2:B:64:GLY:HA2	2:B:242:ASP:HB2	1.90	0.52
2:B:112:GLY:HA3	2:B:893:ASN:HB3	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:1072:GLY:H	2:B:1075:GLU:CD	2.13	0.52
3:C:272:LYS:HD3	14:N:179:ASP:HB3	1.91	0.52
15:O:235:GLU:CA	15:O:237:ILE:HB	2.40	0.52
15:O:374:PRO:O	15:O:376:TYR:CD2	2.63	0.52
16:P:414:ILE:HB	16:P:425:GLY:O	2.10	0.52
16:P:452:THR:HG21	16:P:508:ILE:HG22	1.92	0.52
17:Q:8:PRO:CG	17:Q:19:LEU:HD23	2.40	0.52
17:Q:22:ILE:HD12	17:Q:26:ARG:CZ	2.40	0.52
17:Q:341:ARG:HH12	17:Q:369:TRP:HE1	1.53	0.52
1:A:436:ALA:HA	1:A:439:ASP:C	2.28	0.51
1:A:466:LEU:HD11	2:B:1181:VAL:CG2	2.41	0.51
1:A:475:ARG:O	2:B:1059:PRO:HD2	2.10	0.51
1:A:1482:LYS:HD3	2:B:304:ASP:CG	2.29	0.51
2:B:1010:ASN:HB3	2:B:1025:ASP:HB3	1.93	0.51
3:C:47:LEU:HD23	3:C:48:ASP:N	2.25	0.51
3:C:142:ARG:NH2	10:J:67:GLU:OE2	2.42	0.51
16:P:382:GLU:OE2	16:P:432:PRO:HG2	2.10	0.51
1:A:1657:LEU:CG	7:G:104:LEU:HD13	2.39	0.51
2:B:16:PHE:CD2	10:J:32:GLU:OE2	2.63	0.51
15:O:223:SER:O	15:O:226:GLY:N	2.35	0.51
16:P:193:LEU:CD1	16:P:251:SER:H	2.23	0.51
16:P:436:ILE:H	18:R:143:THR:H	1.59	0.51
17:Q:351:ASN:CG	17:Q:369:TRP:CE2	2.83	0.51
1:A:476:VAL:CG2	2:B:1069:ILE:N	2.73	0.51
1:A:477:ASN:CG	2:B:1047:ARG:NH1	2.56	0.51
1:A:1050:TYR:CE1	1:A:1185:VAL:CG1	2.93	0.51
1:A:1574:ALA:C	9:I:122:ARG:NH1	2.62	0.51
1:A:1575:ILE:CD1	9:I:122:ARG:NH1	2.64	0.51
1:A:1657:LEU:O	6:F:132:LEU:HA	2.09	0.51
15:O:240:ILE:HG22	15:O:380:SER:OG	2.04	0.51
16:P:317:ILE:HD11	16:P:326:ILE:HG23	1.92	0.51
16:P:426:ALA:O	16:P:433:VAL:HG11	2.10	0.51
12:L:28:LYS:O	12:L:59:ALA:N	2.40	0.51
16:P:384:ASP:HB3	16:P:389:TRP:CD1	2.45	0.51
18:R:4:VAL:HG11	18:R:214:VAL:CG2	2.40	0.51
18:R:177:LEU:HD22	18:R:185:LYS:CG	2.37	0.51
18:R:206:ARG:HH21	18:R:211:ARG:NH1	2.05	0.51
1:A:435:ASN:HB3	1:A:442:LYS:C	2.29	0.51
2:B:49:PHE:CD2	2:B:194:PHE:CZ	2.95	0.51
2:B:497:ILE:HG13	2:B:699:ILE:CD1	2.40	0.51
16:P:217:ALA:O	16:P:219:LEU:N	2.43	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:P:294:PHE:HB2	16:P:296:GLU:H	1.75	0.51
16:P:438:TRP:CD1	18:R:141:TRP:CH2	2.97	0.51
1:A:1450:ILE:HD12	1:A:1460:TYR:CD2	2.46	0.51
15:O:240:ILE:CG2	15:O:332:LEU:HD11	2.41	0.51
17:Q:447:ALA:HA	17:Q:450:THR:HB	1.91	0.51
1:A:966:LEU:HD21	1:A:997:PHE:HE1	1.62	0.51
2:B:25:PHE:CZ	10:J:59:LYS:HD2	2.44	0.51
2:B:864:ASP:CB	17:Q:412:LYS:NZ	2.74	0.51
16:P:368:HIS:CB	16:P:411:LYS:HZ2	2.23	0.51
17:Q:413:LEU:CD2	18:R:273:TRP:CZ2	2.94	0.51
18:R:269:ASP:N	18:R:269:ASP:OD2	2.43	0.51
1:A:40:ASN:OD1	1:A:40:ASN:N	2.44	0.51
1:A:507:TYR:HD1	1:A:509:GLU:HG2	1.76	0.51
2:B:532:HIS:NE2	2:B:723:LYS:CE	2.73	0.51
4:D:48:GLU:OE2	4:D:90:LYS:NZ	2.43	0.51
16:P:272:PHE:HE1	16:P:303:VAL:HB	1.75	0.51
16:P:420:GLU:HA	16:P:442:LEU:HD22	1.93	0.51
16:P:625:ASP:O	16:P:629:ARG:HB2	2.11	0.51
17:Q:10:CYS:HB2	17:Q:17:SER:N	2.25	0.51
17:Q:382:GLU:HB2	18:R:241:ARG:HH11	1.75	0.51
1:A:1482:LYS:CE	2:B:304:ASP:CG	2.64	0.51
2:B:212:ASN:ND2	2:B:361:HIS:CG	2.79	0.51
15:O:591:TYR:CE2	15:O:593:PRO:HG3	2.46	0.51
16:P:422:ILE:HG12	16:P:442:LEU:HD12	1.93	0.51
1:A:588:LEU:HD21	2:B:1087:LEU:CD1	2.31	0.51
1:A:953:GLU:C	1:A:1205:PHE:HB3	2.27	0.51
15:O:144:CYS:HB2	15:O:179:PHE:CZ	2.46	0.51
16:P:442:LEU:HD13	16:P:442:LEU:N	2.26	0.51
16:P:573:GLU:HB3	17:Q:499:LYS:HD3	1.93	0.51
1:A:597:LYS:HD2	2:B:1082:HIS:CG	2.46	0.50
1:A:721:LYS:HZ1	8:H:91:ASP:HA	1.74	0.50
1:A:840:ASN:O	1:A:844:THR:HG23	2.11	0.50
1:A:986:PHE:CD2	2:B:958:MET:HE2	2.46	0.50
2:B:679:GLN:CD	14:N:156:PRO:C	2.65	0.50
17:Q:313:THR:O	17:Q:317:MET:HB2	2.11	0.50
17:Q:414:TYR:HD1	18:R:240:ILE:HG13	1.74	0.50
1:A:1573:TYR:HA	9:I:111:PHE:HE2	1.76	0.50
2:B:68:ILE:HD13	2:B:418:ASP:OD1	2.12	0.50
2:B:819:ASP:CG	2:B:820:PRO:HD2	2.31	0.50
2:B:858:ILE:HD13	2:B:872:LYS:O	2.11	0.50
2:B:1089:GLN:HB3	2:B:1093:LEU:HD22	1.91	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:O:378:THR:O	15:O:379:ARG:NH1	2.44	0.50
16:P:253:SER:HA	16:P:261:VAL:HG11	1.94	0.50
16:P:414:ILE:HB	16:P:425:GLY:C	2.32	0.50
16:P:436:ILE:CG2	18:R:143:THR:N	2.57	0.50
16:P:603:ARG:O	16:P:607:VAL:HG23	2.12	0.50
1:A:408:LYS:CD	1:A:408:LYS:N	2.73	0.50
1:A:991:LYS:CA	1:A:994:GLU:HG3	2.39	0.50
15:O:240:ILE:HG23	15:O:332:LEU:CG	2.41	0.50
15:O:507:GLN:O	15:O:511:ILE:HG23	2.12	0.50
1:A:597:LYS:HD3	2:B:1082:HIS:N	2.27	0.50
1:A:953:GLU:C	1:A:1205:PHE:HB2	2.24	0.50
1:A:991:LYS:N	1:A:994:GLU:N	2.58	0.50
1:A:1025:LYS:NZ	2:B:1076:ARG:HH12	2.09	0.50
2:B:202:LEU:H	2:B:202:LEU:CD2	2.13	0.50
15:O:200:ASN:OD1	17:Q:14:ASN:HB2	2.01	0.50
15:O:216:LEU:HD13	15:O:342:HIS:CB	2.41	0.50
15:O:591:TYR:HE2	15:O:593:PRO:HG3	1.77	0.50
16:P:656:HIS:CE1	16:P:748:GLU:HG3	2.47	0.50
16:P:767:PRO:O	16:P:771:ILE:HG12	2.11	0.50
17:Q:10:CYS:SG	17:Q:29:CYS:SG	3.07	0.50
17:Q:303:GLU:O	17:Q:306:VAL:N	2.44	0.50
17:Q:355:VAL:HB	18:R:212:HIS:HE1	1.75	0.50
17:Q:414:TYR:CE2	17:Q:419:LEU:HB3	2.45	0.50
1:A:435:ASN:CA	1:A:442:LYS:HB2	2.42	0.50
1:A:827:THR:CG2	1:A:924:SER:CB	2.90	0.50
1:A:970:LYS:HG2	1:A:973:GLU:HG2	1.92	0.50
1:A:1484:LEU:HD22	2:B:305:ARG:HH21	1.76	0.50
2:B:293:ILE:HG12	2:B:306:LEU:HD13	1.94	0.50
2:B:1005:TYR:CE2	14:N:170:HIS:CD2	2.99	0.50
10:J:1:MET:HG2	10:J:57:ILE:HB	1.93	0.50
15:O:236:LYS:N	15:O:237:ILE:CD1	2.75	0.50
16:P:433:VAL:C	18:R:145:SER:HA	2.31	0.50
16:P:658:LYS:CB	16:P:660:LYS:H	2.24	0.50
17:Q:118:TRP:CZ2	17:Q:189:LYS:HB3	2.47	0.50
1:A:597:LYS:HD2	2:B:1082:HIS:CE1	2.47	0.50
2:B:943:ILE:CD1	10:J:44:TYR:CD1	2.93	0.50
3:C:272:LYS:CA	14:N:175:TYR:CE2	2.83	0.50
9:I:91:ASN:OD1	9:I:92:GLU:N	2.45	0.50
15:O:324:GLY:O	15:O:326:LYS:N	2.44	0.50
16:P:443:ASP:HB3	18:R:3:GLU:HB2	1.93	0.50
18:R:6:ILE:CG1	18:R:213:ILE:HG22	2.40	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:R:364:VAL:HA	18:R:367:ILE:HB	1.93	0.50
2:B:531:VAL:HG13	2:B:716:MET:CA	2.41	0.50
2:B:1003:ALA:C	14:N:169:GLU:H	2.15	0.50
3:C:37:LYS:HG3	11:K:134:LYS:NZ	2.27	0.50
5:E:145:THR:C	5:E:147:HIS:N	2.65	0.50
16:P:363:ILE:HG22	16:P:374:VAL:HG22	1.93	0.50
16:P:390:GLN:O	18:R:149:LYS:CB	2.56	0.50
16:P:498:LEU:HD23	16:P:499:GLU:H	1.75	0.50
18:R:85:ARG:HH11	18:R:85:ARG:HG2	1.77	0.50
1:A:486:PRO:O	2:B:781:TYR:HD2	1.85	0.50
1:A:1298:ASP:CB	1:A:1468:LYS:HZ3	2.24	0.50
1:A:1323:HIS:N	1:A:1454:HIS:NE2	2.60	0.50
2:B:656:LEU:HD22	14:N:153:VAL:CG2	2.42	0.50
2:B:682:GLN:N	14:N:154:ARG:HH21	2.03	0.50
3:C:47:LEU:HD23	3:C:48:ASP:H	1.77	0.50
15:O:468:GLU:C	15:O:470:PHE:H	2.15	0.50
15:O:515:ASN:HD21	15:O:547:ASN:ND2	2.10	0.50
17:Q:24:ASP:CG	17:Q:26:ARG:HE	2.14	0.50
1:A:395:LEU:HD11	18:R:410:TYR:CE1	2.47	0.50
1:A:476:VAL:CG2	2:B:1070:ARG:H	2.05	0.50
1:A:1575:ILE:H	9:I:122:ARG:NH1	2.03	0.50
2:B:545:PHE:CE1	2:B:649:MET:SD	3.04	0.50
16:P:435:ARG:NH2	18:R:140:ILE:HD12	2.26	0.50
16:P:768:TYR:O	16:P:771:ILE:HB	2.12	0.50
17:Q:417:PHE:HZ	18:R:270:PHE:CB	2.25	0.50
1:A:425:ASN:HD22	18:R:405:ILE:HG21	1.71	0.49
2:B:225:ARG:NH2	2:B:261:ARG:HD3	2.27	0.49
2:B:262:PHE:CD1	2:B:357:ILE:HD13	2.47	0.49
15:O:248:LEU:HB2	15:O:598:PHE:CE2	2.47	0.49
16:P:194:ARG:NH2	16:P:208:GLY:HA3	2.27	0.49
16:P:274:ILE:HD13	16:P:305:PHE:HZ	1.76	0.49
16:P:681:GLN:HA	16:P:684:GLN:HB2	1.93	0.49
17:Q:413:LEU:HA	17:Q:416:ILE:HD12	1.94	0.49
18:R:231:LEU:O	18:R:235:ILE:HG12	2.12	0.49
18:R:361:ASP:C	18:R:363:GLU:H	2.14	0.49
1:A:544:VAL:CG1	17:Q:32:GLY:O	2.57	0.49
2:B:535:ASP:N	2:B:720:GLN:OE1	2.43	0.49
2:B:679:GLN:NE2	14:N:155:VAL:O	2.45	0.49
2:B:1090:ASP:OD1	2:B:1094:ASN:ND2	2.43	0.49
7:G:47:VAL:HB	7:G:65:HIS:CD2	2.47	0.49
16:P:441:ASP:HA	16:P:442:LEU:HD13	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:P:489:PHE:CD2	18:R:138:PHE:HZ	2.29	0.49
17:Q:188:ALA:O	17:Q:384:GLN:HG3	2.11	0.49
18:R:372:HIS:CD2	18:R:410:TYR:HB3	2.47	0.49
1:A:437:PHE:HA	1:A:455:GLY:HA3	1.93	0.49
1:A:467:PHE:CD2	1:A:1614:SER:HB3	2.46	0.49
1:A:689:ARG:HD2	8:H:79:TRP:HZ3	1.76	0.49
6:F:72:LYS:HD3	6:F:142:SER:CB	2.28	0.49
17:Q:137:TRP:O	17:Q:141:LEU:HB2	2.12	0.49
18:R:361:ASP:HB3	18:R:364:VAL:HG13	1.94	0.49
1:A:408:LYS:N	1:A:408:LYS:CE	2.75	0.49
1:A:720:PHE:CE1	8:H:98:TYR:HB2	2.47	0.49
1:A:966:LEU:HD21	1:A:997:PHE:CZ	2.36	0.49
1:A:1148:LEU:HD22	1:A:1163:GLU:HG3	1.93	0.49
2:B:550:ARG:HG2	2:B:650:LEU:O	2.12	0.49
15:O:518:LYS:NZ	15:O:575:SER:HB2	2.27	0.49
16:P:22:GLY:HA3	18:R:139:GLU:OE2	2.05	0.49
16:P:365:TRP:CB	16:P:372:ILE:HA	2.42	0.49
17:Q:188:ALA:HB1	17:Q:384:GLN:CG	2.20	0.49
1:A:507:TYR:HE1	1:A:510:PRO:HD3	1.77	0.49
1:A:828:CYS:SG	2:B:1027:TYR:HB2	2.53	0.49
2:B:29:PRO:O	2:B:177:PRO:HB2	2.11	0.49
6:F:73:ALA:CA	6:F:143:PHE:O	2.56	0.49
15:O:376:TYR:CB	15:O:419:LYS:HD3	2.43	0.49
15:O:379:ARG:NH1	15:O:379:ARG:CA	2.73	0.49
16:P:599:LYS:HG2	17:Q:272:GLN:OE1	2.13	0.49
17:Q:417:PHE:CE2	18:R:253:ILE:HD13	2.47	0.49
1:A:861:VAL:HG21	1:A:892:LEU:HA	1.93	0.49
1:A:1658:ALA:CA	6:F:131:PRO:O	2.58	0.49
2:B:25:PHE:CG	10:J:59:LYS:CG	2.96	0.49
2:B:743:ARG:CZ	10:J:60:PHE:HZ	2.23	0.49
2:B:1073:GLU:HA	2:B:1076:ARG:HB2	1.95	0.49
3:C:58:ASN:N	3:C:296:ASN:ND2	2.58	0.49
3:C:117:ASP:OD1	3:C:119:ASN:ND2	2.44	0.49
13:M:103:LYS:HA	13:M:106:LYS:HB2	1.93	0.49
15:O:248:LEU:CG	15:O:598:PHE:CD2	2.90	0.49
15:O:428:ILE:CD1	15:O:442:VAL:HG21	2.42	0.49
15:O:436:ARG:HG3	15:O:490:ILE:HG23	1.95	0.49
16:P:225:LEU:HD11	16:P:235:SER:HB3	1.93	0.49
16:P:446:ASP:OD2	16:P:448:THR:N	2.40	0.49
18:R:177:LEU:CD2	18:R:185:LYS:HA	2.43	0.49
1:A:410:LYS:CB	1:A:411:VAL:HG23	2.43	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:425:ASN:ND2	18:R:406:LYS:HZ3	2.09	0.49
1:A:514:TYR:O	6:F:115:THR:HG22	2.12	0.49
1:A:1482:LYS:CD	2:B:304:ASP:CG	2.81	0.49
2:B:551:ILE:HG23	2:B:647:SER:C	2.29	0.49
8:H:26:ILE:HD12	8:H:42:ILE:HD12	1.93	0.49
13:M:65:TYR:CE1	13:M:97:VAL:HB	2.48	0.49
15:O:474:TYR:HB3	15:O:520:CYS:SG	2.53	0.49
16:P:49:THR:O	16:P:49:THR:OG1	2.27	0.49
17:Q:10:CYS:HB3	17:Q:16:PRO:HA	1.93	0.49
1:A:629:ASP:O	2:B:926:VAL:CG2	2.55	0.49
1:A:1657:LEU:O	6:F:132:LEU:C	2.49	0.49
2:B:30:LYS:O	2:B:176:SER:HB3	2.13	0.49
2:B:207:ILE:CG1	2:B:503:VAL:HG22	2.13	0.49
2:B:679:GLN:OE1	14:N:157:ARG:CB	2.61	0.49
3:C:230:LEU:HD22	3:C:297:HIS:NE2	2.28	0.49
8:H:112:ILE:HD12	8:H:129:TYR:HB2	1.94	0.49
16:P:480:VAL:HB	16:P:492:LEU:CD2	2.40	0.49
1:A:509:GLU:CG	1:A:579:ARG:HE	2.26	0.49
1:A:1055:ILE:HD11	1:A:1174:TYR:CE1	2.48	0.49
1:A:1317:ILE:HB	1:A:1460:TYR:OH	2.13	0.49
2:B:202:LEU:CD1	2:B:499:HIS:HB3	2.40	0.49
2:B:1066:HIS:NE2	17:Q:23:ILE:HD13	2.27	0.49
7:G:24:VAL:O	7:G:128:GLN:HB3	2.04	0.49
15:O:208:LEU:O	15:O:212:THR:HG23	2.12	0.49
16:P:499:GLU:OE1	16:P:499:GLU:HA	2.13	0.49
16:P:757:GLN:HE21	16:P:758:ASN:N	2.10	0.49
17:Q:108:PHE:CZ	17:Q:156:LEU:HD22	2.47	0.49
17:Q:161:THR:OG1	17:Q:162:ILE:N	2.46	0.49
1:A:563:THR:HG22	15:O:375:THR:CG2	2.42	0.49
1:A:671:GLN:HB3	2:B:952:HIS:CE1	2.48	0.49
2:B:62:ASN:OD1	2:B:102:VAL:CG2	2.60	0.49
2:B:143:TRP:CZ2	2:B:446:MET:HG3	2.47	0.49
2:B:162:PRO:HG2	2:B:465:LEU:HD12	1.95	0.49
2:B:338:PHE:CE1	2:B:353:VAL:HG22	2.47	0.49
6:F:66:ARG:HH22	7:G:90:LEU:HB3	1.77	0.49
15:O:336:LEU:HD13	15:O:602:TYR:CE1	2.48	0.49
16:P:197:ARG:HD2	16:P:261:VAL:O	2.12	0.49
16:P:226:HIS:CE1	16:P:234:THR:HG22	2.48	0.49
18:R:361:ASP:O	18:R:363:GLU:N	2.40	0.49
2:B:203:ILE:HG22	2:B:405:GLY:CA	2.42	0.48
3:C:157:TYR:HB2	3:C:160:ALA:HB2	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:P:420:GLU:HG2	16:P:441:ASP:HB2	1.95	0.48
17:Q:152:LEU:HD12	17:Q:154:LEU:HD11	1.95	0.48
17:Q:414:TYR:HE2	17:Q:419:LEU:HB3	1.78	0.48
1:A:563:THR:HG22	15:O:375:THR:HG22	1.95	0.48
1:A:1657:LEU:CD2	7:G:104:LEU:HB3	2.38	0.48
2:B:68:ILE:HD13	2:B:71:LYS:NZ	2.29	0.48
2:B:985:ILE:C	14:N:160:VAL:CG2	2.80	0.48
10:J:6:ARG:HD2	10:J:11:GLY:O	2.13	0.48
15:O:361:PHE:CE2	15:O:365:THR:HG21	2.48	0.48
15:O:468:GLU:C	15:O:470:PHE:N	2.65	0.48
16:P:59:ILE:HG22	16:P:60:VAL:H	1.78	0.48
18:R:206:ARG:N	18:R:206:ARG:NE	2.60	0.48
1:A:68:ASP:O	1:A:70:LYS:N	2.46	0.48
1:A:597:LYS:HB3	2:B:1082:HIS:CD2	2.42	0.48
1:A:1603:MET:HE1	1:A:1615:TYR:CD2	2.46	0.48
2:B:25:PHE:CE2	10:J:59:LYS:HG3	2.48	0.48
16:P:21:GLN:C	18:R:139:GLU:OE2	2.49	0.48
16:P:264:ILE:HG12	16:P:265:THR:N	2.27	0.48
16:P:443:ASP:CB	18:R:3:GLU:CB	2.90	0.48
17:Q:7:GLY:HA3	17:Q:8:PRO:HD2	1.44	0.48
1:A:747:ILE:HD13	1:A:748:ASN:H	1.77	0.48
2:B:1071:VAL:C	2:B:1075:GLU:HG3	2.27	0.48
3:C:215:ASP:CG	12:L:70:ARG:HH22	2.17	0.48
15:O:198:PHE:CZ	15:O:236:LYS:HG3	2.48	0.48
15:O:202:ASN:HB3	17:Q:31:TYR:HH	1.75	0.48
2:B:211:ARG:NH2	2:B:646:HIS:O	2.47	0.48
3:C:326:GLU:HG3	11:K:125:MET:CE	2.40	0.48
16:P:733:THR:HA	16:P:736:ILE:HG22	1.95	0.48
1:A:824:THR:C	2:B:1023:ARG:H	2.08	0.48
1:A:1329:ILE:HG21	1:A:1456:PHE:CD2	2.40	0.48
5:E:48:ASP:OD1	5:E:50:MET:HB3	2.13	0.48
7:G:158:LYS:CB	15:O:105:ASN:OD1	2.61	0.48
15:O:181:ARG:CG	15:O:181:ARG:NH1	2.77	0.48
16:P:186:TYR:OH	18:R:196:GLU:OE1	2.29	0.48
3:C:293:ARG:O	3:C:295:ARG:HD3	2.14	0.48
6:F:70:LYS:CG	7:G:95:LEU:CD2	2.90	0.48
16:P:315:PHE:HB2	16:P:365:TRP:HH2	1.78	0.48
16:P:399:TRP:HZ3	18:R:291:ARG:O	1.92	0.48
16:P:476:ILE:HD12	16:P:508:ILE:HD11	1.96	0.48
16:P:662:LEU:HB3	16:P:665:ASN:CG	2.33	0.48
16:P:762:ARG:HG3	17:Q:139:LYS:HE3	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:478:TYR:CE1	2:B:1049:THR:HB	2.49	0.48
1:A:826:PHE:CE1	2:B:777:SER:OG	2.66	0.48
1:A:869:PRO:HG2	1:A:872:ASP:HB2	1.96	0.48
1:A:1162:ASN:ND2	1:A:1165:LYS:HG3	2.29	0.48
1:A:1297:PHE:HD2	9:I:60:LEU:HD13	1.75	0.48
1:A:1312:GLU:O	1:A:1316:VAL:HG23	2.13	0.48
1:A:1322:ILE:CB	1:A:1454:HIS:CD2	2.85	0.48
1:A:1538:VAL:HG21	5:E:142:VAL:CG2	2.43	0.48
2:B:28:PRO:CD	10:J:62:ARG:NE	2.76	0.48
2:B:1047:ARG:HD3	2:B:1049:THR:O	2.14	0.48
5:E:61:GLN:HE21	5:E:105:PHE:HE1	1.62	0.48
5:E:131:THR:HG21	5:E:191:LYS:CE	2.44	0.48
7:G:23:GLN:O	7:G:25:THR:N	2.46	0.48
7:G:137:ILE:HG13	7:G:227:GLY:O	2.13	0.48
7:G:139:ILE:HD13	15:O:145:SER:OG	2.14	0.48
15:O:199:PRO:HB2	15:O:208:LEU:HD23	1.95	0.48
15:O:521:ASN:O	15:O:525:MET:HG2	2.12	0.48
16:P:277:VAL:HG23	16:P:286:VAL:HG12	1.95	0.48
1:A:19:LEU:HD11	2:B:1190:SER:HB2	1.96	0.48
1:A:410:LYS:CB	1:A:411:VAL:CG2	2.91	0.48
1:A:505:LEU:O	1:A:580:HIS:HA	2.14	0.48
1:A:826:PHE:CD2	1:A:827:THR:N	2.82	0.48
1:A:934:LYS:HG2	2:B:955:PRO:HG2	1.96	0.48
2:B:54:GLU:HG3	2:B:168:ASN:ND2	2.29	0.48
2:B:202:LEU:N	2:B:202:LEU:CD2	2.76	0.48
2:B:413:LEU:O	2:B:417:ILE:HG13	2.14	0.48
2:B:584:CYS:HB3	2:B:596:VAL:HG23	1.95	0.48
2:B:1092:LEU:C	2:B:1096:SER:CB	2.82	0.48
15:O:342:HIS:HE1	15:O:346:GLN:HE21	1.58	0.48
15:O:477:PHE:CE2	15:O:481:CYS:SG	3.07	0.48
18:R:9:THR:O	18:R:13:PHE:HD2	1.97	0.48
1:A:1603:MET:SD	1:A:1612:LYS:HA	2.54	0.48
2:B:1005:TYR:CE2	14:N:170:HIS:ND1	2.82	0.48
3:C:239:ILE:HG23	3:C:243:SER:HB3	1.96	0.48
16:P:290:GLU:HG3	16:P:291:PRO:O	2.14	0.48
16:P:300:LEU:HA	16:P:320:ILE:HG22	1.96	0.48
16:P:427:SER:HA	16:P:433:VAL:HB	1.95	0.48
16:P:770:ASP:HB2	17:Q:145:ASN:OD1	2.14	0.48
1:A:1260:LYS:CE	1:A:1262:LEU:HD21	2.44	0.47
2:B:475:GLY:O	2:B:476:LEU:CB	2.59	0.47
6:F:73:ALA:CA	6:F:143:PHE:CG	2.91	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:P:244:SER:CB	16:P:268:SER:HG	2.27	0.47
18:R:4:VAL:HG21	18:R:214:VAL:CB	2.40	0.47
1:A:477:ASN:HA	2:B:1047:ARG:CD	2.42	0.47
1:A:959:VAL:HG22	1:A:965:THR:HG22	1.95	0.47
1:A:999:CYS:SG	2:B:712:SER:HB3	2.54	0.47
1:A:1050:TYR:HB3	1:A:1054:ALA:CA	2.43	0.47
1:A:1298:ASP:O	1:A:1300:ASN:N	2.47	0.47
2:B:152:LEU:HD22	2:B:443:LYS:CE	2.43	0.47
12:L:45:ALA:O	12:L:47:ARG:N	2.46	0.47
16:P:333:PHE:CD2	16:P:334:ASN:HB2	2.49	0.47
1:A:718:THR:HG21	8:H:118:PHE:O	2.14	0.47
2:B:53:THR:HG21	2:B:104:ILE:HD12	1.95	0.47
2:B:1090:ASP:CA	2:B:1093:LEU:HB3	2.36	0.47
14:N:111:VAL:HG13	14:N:122:ALA:HB2	1.96	0.47
15:O:386:PHE:HB2	15:O:594:TYR:CE2	2.49	0.47
17:Q:22:ILE:HD11	17:Q:26:ARG:CG	2.44	0.47
18:R:15:GLN:OE1	18:R:181:THR:HG23	2.14	0.47
18:R:82:ARG:HD2	18:R:82:ARG:O	2.14	0.47
18:R:162:PHE:HA	18:R:165:ILE:HD12	1.95	0.47
1:A:641:GLU:HB2	6:F:99:LEU:CD1	2.44	0.47
1:A:862:THR:O	9:I:67:VAL:HA	2.14	0.47
1:A:991:LYS:HA	1:A:992:PRO:N	2.29	0.47
2:B:415:GLU:OE2	2:B:472:SER:HB2	2.13	0.47
2:B:1005:TYR:HH	10:J:44:TYR:HD2	1.52	0.47
16:P:185:GLN:HE22	18:R:197:PRO:HB3	1.78	0.47
16:P:227:LEU:HD13	16:P:227:LEU:H	1.78	0.47
17:Q:287:TRP:CE2	17:Q:289:ARG:HB3	2.50	0.47
18:R:11:ARG:H	18:R:11:ARG:HG3	1.53	0.47
1:A:456:VAL:HG13	2:B:1188:GLU:OE1	2.14	0.47
1:A:508:PRO:HD2	1:A:639:GLN:HG3	1.95	0.47
1:A:999:CYS:N	2:B:712:SER:HB3	2.28	0.47
2:B:975:HIS:CE1	14:N:169:GLU:HG3	2.49	0.47
2:B:1151:ILE:HG12	7:G:21:LYS:HZ3	1.77	0.47
13:M:102:SER:CA	13:M:105:SER:H	2.28	0.47
15:O:124:LYS:HD3	15:O:127:GLU:OE2	2.13	0.47
15:O:245:GLN:O	15:O:248:LEU:N	2.40	0.47
16:P:68:THR:HG23	16:P:214:LEU:HA	1.95	0.47
16:P:184:SER:C	18:R:198:LEU:HB3	2.34	0.47
17:Q:250:GLN:OE1	17:Q:271:LYS:HD2	2.15	0.47
1:A:425:ASN:HD21	18:R:406:LYS:NZ	2.11	0.47
1:A:486:PRO:CD	2:B:928:SER:OG	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:747:ILE:HD13	1:A:748:ASN:N	2.29	0.47
1:A:1574:ALA:HB1	9:I:121:PHE:HA	1.95	0.47
4:D:46:GLU:OE1	4:D:47:LYS:HE2	2.15	0.47
15:O:376:TYR:CD1	15:O:419:LYS:HG2	2.49	0.47
17:Q:356:VAL:CB	18:R:208:TYR:HD1	2.27	0.47
1:A:410:LYS:HB3	1:A:411:VAL:HG22	1.96	0.47
1:A:436:ALA:HA	1:A:440:SER:CA	2.44	0.47
1:A:476:VAL:HG11	2:B:1071:VAL:HG23	1.96	0.47
1:A:507:TYR:CD1	1:A:509:GLU:HG2	2.50	0.47
1:A:720:PHE:N	8:H:96:VAL:O	2.46	0.47
1:A:990:ILE:C	1:A:994:GLU:CB	2.82	0.47
1:A:1049:MET:HG3	1:A:1053:ASP:H	1.76	0.47
1:A:1317:ILE:CG2	1:A:1460:TYR:CZ	2.96	0.47
2:B:182:GLN:HE22	10:J:69:ARG:CB	2.08	0.47
2:B:208:VAL:CG2	2:B:401:GLU:CG	2.92	0.47
2:B:338:PHE:CZ	2:B:357:ILE:HD12	2.49	0.47
2:B:1047:ARG:CD	2:B:1049:THR:O	2.60	0.47
3:C:247:PHE:HE1	3:C:289:VAL:HG21	1.80	0.47
6:F:93:ILE:HA	6:F:93:ILE:HD13	1.70	0.47
7:G:144:HIS:HB3	15:O:146:SER:HB3	1.97	0.47
15:O:206:ARG:HA	15:O:209:VAL:CG1	2.45	0.47
15:O:376:TYR:CE2	15:O:419:LYS:HE2	2.50	0.47
16:P:388:ASN:HB3	18:R:151:PRO:HB3	1.97	0.47
16:P:422:ILE:HG12	16:P:442:LEU:HD11	1.96	0.47
16:P:443:ASP:CB	18:R:3:GLU:HB3	2.43	0.47
18:R:198:LEU:HD12	18:R:199:LYS:HB2	1.95	0.47
1:A:1484:LEU:HD11	2:B:305:ARG:HD3	1.97	0.47
2:B:470:LEU:HD21	2:B:476:LEU:HD12	1.97	0.47
2:B:841:ASP:OD1	2:B:842:GLU:N	2.40	0.47
3:C:292:GLY:CA	3:C:295:ARG:HH22	2.27	0.47
7:G:156:SER:OG	15:O:146:SER:HA	2.13	0.47
15:O:91:LYS:HG3	15:O:92:ASN:N	2.28	0.47
16:P:56:ASP:OD1	16:P:554:ASN:ND2	2.48	0.47
16:P:185:GLN:HB3	18:R:195:LEU:C	2.34	0.47
16:P:381:ILE:HA	16:P:391:THR:O	2.14	0.47
16:P:421:ILE:CG2	16:P:423:ILE:HG13	2.44	0.47
17:Q:371:GLU:HG3	18:R:231:LEU:CG	2.45	0.47
1:A:1032:VAL:HG22	1:A:1050:TYR:HD1	1.75	0.47
1:A:1258:ILE:HB	1:A:1501:ILE:HD12	1.97	0.47
4:D:33:THR:HG23	4:D:96:PHE:HD1	1.80	0.47
16:P:290:GLU:OE2	16:P:291:PRO:HD2	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:Q:414:TYR:CE1	18:R:240:ILE:HG23	2.44	0.47
17:Q:417:PHE:CZ	18:R:270:PHE:HB2	2.47	0.47
1:A:990:ILE:CB	1:A:994:GLU:HB3	2.07	0.47
1:A:995:TYR:HH	2:B:707:SER:CB	1.88	0.47
2:B:736:ARG:HD3	2:B:738:ASP:OD2	2.15	0.47
6:F:69:LEU:HG	6:F:143:PHE:HE2	1.80	0.47
15:O:240:ILE:CG2	15:O:332:LEU:CD1	2.93	0.47
15:O:243:GLU:HG2	15:O:332:LEU:HB2	1.97	0.47
16:P:330:PRO:HG3	16:P:342:GLN:CG	2.45	0.47
17:Q:193:PHE:HE2	18:R:208:TYR:CZ	2.32	0.47
17:Q:197:GLU:HG3	17:Q:388:THR:O	2.14	0.47
1:A:721:LYS:HB3	8:H:96:VAL:CB	2.40	0.46
1:A:1482:LYS:HD3	2:B:304:ASP:HA	1.97	0.46
1:A:1655:ASP:CB	6:F:135:ARG:HB3	2.38	0.46
2:B:535:ASP:CG	2:B:720:GLN:HE22	2.17	0.46
2:B:1103:VAL:HG22	2:B:1176:VAL:HG22	1.97	0.46
16:P:272:PHE:HB2	16:P:300:LEU:HD11	1.97	0.46
16:P:626:LEU:HD22	16:P:626:LEU:HA	1.59	0.46
17:Q:235:GLY:HA3	17:Q:287:TRP:CD1	2.50	0.46
18:R:30:ARG:NE	18:R:168:ILE:HD12	2.30	0.46
2:B:265:ARG:NH2	2:B:339:GLN:OE1	2.48	0.46
2:B:407:PHE:HE2	2:B:647:SER:OG	1.98	0.46
2:B:812:ALA:HA	2:B:815:ARG:HD3	1.96	0.46
2:B:943:ILE:HD13	10:J:44:TYR:CE1	2.47	0.46
15:O:409:ALA:HB3	15:O:412:GLU:HG3	1.97	0.46
16:P:438:TRP:HE1	18:R:297:PHE:HZ	1.63	0.46
16:P:443:ASP:OD2	18:R:3:GLU:OE2	2.33	0.46
18:R:6:ILE:CG1	18:R:213:ILE:CG2	2.93	0.46
18:R:402:ASN:O	18:R:406:LYS:HG2	2.15	0.46
1:A:474:LYS:NZ	2:B:1096:SER:HB2	2.30	0.46
1:A:1276:THR:H	9:I:45:LEU:C	2.11	0.46
1:A:1440:ASN:HA	1:A:1443:GLN:HB2	1.96	0.46
2:B:397:THR:HA	2:B:400:GLN:OE1	2.14	0.46
2:B:549:CYS:SG	2:B:649:MET:CB	3.03	0.46
6:F:72:LYS:CG	6:F:142:SER:CA	2.91	0.46
14:N:87:TYR:CE2	14:N:141:GLU:CD	2.88	0.46
15:O:468:GLU:O	15:O:470:PHE:N	2.49	0.46
16:P:366:PHE:HE2	16:P:433:VAL:H	1.64	0.46
16:P:437:SER:CB	18:R:140:ILE:HD13	2.45	0.46
17:Q:9:ILE:CG1	17:Q:10:CYS:N	2.50	0.46
17:Q:274:ILE:HG23	17:Q:282:ARG:NH2	2.29	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:Q:309:TYR:O	17:Q:313:THR:OG1	2.20	0.46
18:R:257:ILE:HG21	18:R:266:SER:HA	1.96	0.46
1:A:472:MET:CB	2:B:1073:GLU:OE1	2.64	0.46
2:B:554:GLN:O	2:B:555:GLN:C	2.54	0.46
2:B:890:ASP:HB3	2:B:896:GLN:OE1	2.16	0.46
5:E:93:MET:CG	5:E:120:ALA:HB1	2.46	0.46
15:O:521:ASN:HD22	15:O:524:VAL:H	1.63	0.46
16:P:408:ILE:HD12	16:P:464:LEU:HD13	1.97	0.46
16:P:770:ASP:OD2	17:Q:141:LEU:HG	2.15	0.46
16:P:778:ASP:CG	16:P:779:ASP:H	2.19	0.46
17:Q:250:GLN:HB3	17:Q:267:TYR:OH	2.15	0.46
18:R:199:LYS:NZ	18:R:204:GLU:CA	2.62	0.46
1:A:475:ARG:HD3	2:B:1060:VAL:O	2.16	0.46
1:A:720:PHE:HB2	8:H:96:VAL:HG12	1.97	0.46
2:B:894:LYS:CG	12:L:47:ARG:CD	2.94	0.46
15:O:240:ILE:HG22	15:O:332:LEU:HD11	1.96	0.46
15:O:390:GLN:NE2	15:O:433:LYS:H	2.13	0.46
16:P:187:ILE:CG2	18:R:195:LEU:CD2	2.92	0.46
16:P:438:TRP:CG	18:R:141:TRP:HZ2	2.30	0.46
18:R:222:LEU:HD23	18:R:226:ARG:NH2	2.31	0.46
1:A:1118:VAL:CG1	5:E:199:ILE:HG13	2.44	0.46
1:A:1662:ASN:C	7:G:101:SER:HB2	2.35	0.46
2:B:407:PHE:HE2	2:B:647:SER:HG	1.64	0.46
2:B:774:ALA:HB1	2:B:1026:ILE:HD11	1.97	0.46
2:B:990:ASP:OD2	14:N:159:ASP:HB3	2.16	0.46
6:F:70:LYS:HD2	7:G:94:PRO:HB2	1.45	0.46
9:I:23:VAL:O	9:I:39:LYS:NZ	2.49	0.46
11:K:49:LEU:HG	11:K:54:THR:HG21	1.98	0.46
15:O:234:ILE:HG21	15:O:367:LEU:HB3	1.96	0.46
15:O:407:SER:HB3	15:O:420:SER:HB2	1.96	0.46
16:P:265:THR:HG1	16:P:305:PHE:HE1	1.61	0.46
16:P:389:TRP:HH2	18:R:148:ASN:HA	1.77	0.46
16:P:428:GLU:O	18:R:142:ARG:NH1	2.46	0.46
16:P:444:PRO:CG	16:P:449:LEU:HD11	2.46	0.46
17:Q:22:ILE:HD13	17:Q:26:ARG:CZ	2.45	0.46
18:R:177:LEU:HD21	18:R:185:LYS:HA	1.98	0.46
1:A:258:GLU:HA	1:A:261:ILE:HD12	1.96	0.46
1:A:597:LYS:HD3	2:B:1081:GLY:C	2.36	0.46
2:B:25:PHE:CG	10:J:59:LYS:HG2	2.51	0.46
6:F:74:ILE:N	7:G:95:LEU:HD11	2.30	0.46
15:O:93:LEU:HD23	15:O:132:THR:CG2	2.46	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:P:321:LYS:HB2	16:P:321:LYS:NZ	2.31	0.46
16:P:574:TRP:CH2	17:Q:495:LYS:HD2	2.51	0.46
17:Q:188:ALA:C	17:Q:384:GLN:HG2	2.35	0.46
17:Q:358:PRO:O	18:R:206:ARG:NH1	2.49	0.46
1:A:1484:LEU:CD2	2:B:304:ASP:HB2	2.46	0.46
2:B:679:GLN:OE1	14:N:157:ARG:CA	2.63	0.46
2:B:848:ILE:CG1	12:L:60:ARG:HD2	2.36	0.46
3:C:176:SER:O	3:C:180:ALA:HB2	2.16	0.46
3:C:293:ARG:O	3:C:295:ARG:CD	2.64	0.46
16:P:54:ALA:HA	16:P:55:LEU:HD12	1.98	0.46
16:P:56:ASP:O	16:P:57:LEU:HD13	2.16	0.46
16:P:197:ARG:CD	16:P:261:VAL:O	2.64	0.46
16:P:417:THR:OG1	16:P:451:ILE:HB	2.16	0.46
17:Q:351:ASN:ND2	17:Q:369:TRP:CE2	2.83	0.46
17:Q:406:GLN:HE21	18:R:282:SER:C	2.18	0.46
18:R:323:SER:OG	18:R:324:MET:N	2.46	0.46
1:A:406:LEU:CB	1:A:408:LYS:HZ2	2.27	0.46
1:A:1574:ALA:HB3	9:I:122:ARG:HG2	1.97	0.46
2:B:292:ILE:HB	2:B:306:LEU:HD11	1.98	0.46
2:B:679:GLN:HG2	14:N:156:PRO:CA	2.33	0.46
2:B:1045:GLN:HB3	2:B:1063:ARG:HG3	1.97	0.46
2:B:1049:THR:CG2	2:B:1050:GLY:N	2.63	0.46
10:J:36:LEU:HD13	10:J:47:ARG:HB3	1.98	0.46
15:O:74:ILE:O	15:O:78:VAL:HG13	2.16	0.46
15:O:169:THR:O	15:O:170:VAL:C	2.54	0.46
16:P:197:ARG:CB	16:P:261:VAL:O	2.63	0.46
16:P:254:ILE:HG21	16:P:368:HIS:CE1	2.50	0.46
16:P:326:ILE:HG21	16:P:385:PHE:CE1	2.51	0.46
17:Q:137:TRP:CH2	17:Q:141:LEU:HD13	2.51	0.46
18:R:365:TRP:HB3	18:R:418:CYS:HB2	1.98	0.46
1:A:582:LYS:O	1:A:585:ASP:HB2	2.16	0.46
1:A:1049:MET:CB	1:A:1052:GLY:N	2.64	0.46
2:B:293:ILE:CD1	2:B:302:LEU:HB3	2.46	0.46
2:B:404:LEU:C	2:B:406:GLY:N	2.66	0.46
2:B:822:THR:HB	2:B:823:GLN:HG3	1.98	0.46
9:I:89:CYS:SG	9:I:91:ASN:HB2	2.56	0.46
15:O:190:ILE:HD13	15:O:190:ILE:C	2.37	0.46
15:O:245:GLN:NE2	15:O:379:ARG:CB	2.74	0.46
15:O:388:VAL:HG13	15:O:389:SER:N	2.31	0.46
16:P:350:THR:HB	18:R:155:GLN:HA	1.98	0.46
16:P:770:ASP:HB2	17:Q:145:ASN:CG	2.36	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:Q:193:PHE:HD2	18:R:208:TYR:CE2	2.31	0.46
1:A:991:LYS:HB3	1:A:993:GLN:CG	2.46	0.45
1:A:1237:GLN:H	1:A:1544:ASN:HB2	1.81	0.45
1:A:1310:LYS:HG2	1:A:1311:GLU:OE1	2.07	0.45
2:B:119:ARG:CZ	12:L:53:HIS:NE2	2.79	0.45
2:B:236:ILE:HG21	2:B:377:MET:HE1	1.97	0.45
2:B:585:CYS:HB2	2:B:595:TRP:CZ3	2.51	0.45
3:C:228:ARG:HH22	14:N:175:TYR:HE2	1.62	0.45
6:F:70:LYS:CE	7:G:95:LEU:CD2	2.82	0.45
15:O:517:LEU:HD23	15:O:525:MET:HE3	1.97	0.45
16:P:580:ASN:HB2	17:Q:506:LYS:HE2	1.98	0.45
17:Q:375:LEU:HD21	18:R:231:LEU:HD23	1.98	0.45
18:R:236:PHE:CZ	18:R:253:ILE:HB	2.51	0.45
1:A:476:VAL:N	2:B:1059:PRO:HG2	2.31	0.45
1:A:489:ASN:CB	11:K:95:HIS:HD2	2.29	0.45
1:A:1053:ASP:O	1:A:1055:ILE:CG1	2.55	0.45
3:C:228:ARG:CD	14:N:173:THR:OG1	2.64	0.45
15:O:69:THR:HG22	15:O:70:GLN:N	2.31	0.45
15:O:517:LEU:HD23	15:O:525:MET:CE	2.46	0.45
16:P:224:THR:HG21	16:P:237:GLU:HA	1.99	0.45
1:A:466:LEU:HD21	2:B:1181:VAL:HG22	1.98	0.45
1:A:514:TYR:CD1	6:F:115:THR:O	2.70	0.45
2:B:54:GLU:OE2	2:B:168:ASN:ND2	2.46	0.45
2:B:1047:ARG:HG2	2:B:1049:THR:H	1.81	0.45
3:C:228:ARG:HG3	3:C:299:ILE:HB	1.98	0.45
15:O:200:ASN:OD1	17:Q:14:ASN:CB	2.61	0.45
16:P:296:GLU:HB3	16:P:298:ASP:OD1	2.16	0.45
17:Q:193:PHE:HA	17:Q:219:ILE:HD11	1.97	0.45
17:Q:356:VAL:HG21	18:R:208:TYR:CE1	2.51	0.45
17:Q:359:ASP:OD2	17:Q:359:ASP:N	2.47	0.45
17:Q:378:LEU:HD11	18:R:235:ILE:HD13	1.96	0.45
17:Q:416:ILE:HD13	18:R:273:TRP:CD1	2.50	0.45
18:R:1:MET:HG3	18:R:2:PHE:CD1	2.51	0.45
1:A:184:LYS:HA	1:A:187:GLU:HG2	1.98	0.45
1:A:403:LEU:HD13	1:A:419:ILE:HG23	1.98	0.45
1:A:414:GLU:C	1:A:416:ARG:N	2.67	0.45
1:A:535:GLN:HE22	17:Q:26:ARG:HG2	1.81	0.45
1:A:1660:VAL:HG23	7:G:103:LYS:H	1.82	0.45
2:B:203:ILE:CB	2:B:405:GLY:HA3	2.46	0.45
2:B:786:ALA:HB1	2:B:928:SER:HB2	1.98	0.45
5:E:7:ARG:O	5:E:11:ARG:HG3	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:O:467:MET:HE1	15:O:470:PHE:HE2	1.81	0.45
15:O:578:SER:O	15:O:579:LEU:CB	2.64	0.45
16:P:498:LEU:HD23	16:P:499:GLU:O	2.16	0.45
17:Q:104:PHE:HZ	17:Q:156:LEU:HB2	1.77	0.45
2:B:894:LYS:HA	12:L:54:ARG:HE	1.77	0.45
16:P:61:VAL:HB	16:P:551:ALA:HB3	1.97	0.45
16:P:198:ASP:OD1	16:P:204:ALA:HB1	2.17	0.45
16:P:428:GLU:HB2	16:P:435:ARG:NH1	2.30	0.45
17:Q:351:ASN:C	17:Q:369:TRP:CH2	2.80	0.45
1:A:474:LYS:NZ	2:B:1092:LEU:CA	2.67	0.45
1:A:1600:ARG:HB2	1:A:1616:GLU:OE2	2.17	0.45
16:P:24:SER:CB	18:R:318:ILE:CD1	2.89	0.45
16:P:196:TYR:HA	16:P:207:SER:O	2.16	0.45
16:P:198:ASP:OD1	16:P:204:ALA:CB	2.64	0.45
16:P:384:ASP:CB	16:P:389:TRP:HB3	2.43	0.45
16:P:728:GLN:HB3	16:P:731:LEU:HB3	1.97	0.45
17:Q:204:ARG:HG3	17:Q:205:ILE:HG13	1.99	0.45
17:Q:286:LEU:CD2	17:Q:300:ASN:HB3	2.47	0.45
1:A:719:ILE:HG12	8:H:97:MET:CG	2.40	0.45
5:E:78:LEU:HD13	5:E:107:THR:HB	1.98	0.45
16:P:394:VAL:HG22	16:P:434:ARG:NH1	2.32	0.45
16:P:454:GLN:HE22	16:P:536:ASP:H	1.65	0.45
17:Q:153:LYS:HE2	17:Q:153:LYS:HB3	1.57	0.45
17:Q:310:PHE:O	17:Q:314:ILE:HG13	2.16	0.45
1:A:615:ARG:HH22	2:B:929:ARG:CG	2.14	0.45
2:B:145:VAL:CG2	2:B:440:PHE:O	2.65	0.45
2:B:679:GLN:OE1	14:N:157:ARG:HA	2.16	0.45
3:C:222:VAL:HB	3:C:224:THR:H	1.81	0.45
16:P:189:THR:HB	16:P:247:ILE:HG23	1.98	0.45
16:P:246:LYS:HB3	16:P:246:LYS:HE3	1.59	0.45
16:P:252:GLU:OE1	16:P:253:SER:N	2.35	0.45
16:P:596:ILE:HD12	16:P:596:ILE:O	2.16	0.45
17:Q:435:GLN:H	17:Q:435:GLN:HG3	1.38	0.45
18:R:295:PRO:HB3	18:R:296:PRO:HD2	1.97	0.45
1:A:89:LEU:HD11	2:B:1192:MET:HB3	1.97	0.45
1:A:407:GLN:CB	1:A:409:ASP:N	2.73	0.45
1:A:653:THR:OG1	1:A:654:ASP:OD1	2.35	0.45
2:B:190:ILE:HG13	2:B:191:GLY:N	2.32	0.45
2:B:548:LYS:O	2:B:550:ARG:NH1	2.50	0.45
13:M:65:TYR:HE1	13:M:97:VAL:HB	1.81	0.45
16:P:193:LEU:HD12	16:P:250:ALA:HA	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:Q:385:PHE:CZ	18:R:209:ARG:HG3	2.52	0.45
1:A:545:SER:HB2	17:Q:34:VAL:HG21	0.50	0.45
1:A:581:ILE:CD1	1:A:637:PHE:CZ	2.97	0.45
15:O:396:MET:HE1	15:O:434:LEU:N	2.31	0.45
15:O:433:LYS:HZ2	15:O:609:TYR:HE1	1.63	0.45
16:P:21:GLN:O	16:P:25:LEU:HB2	2.17	0.45
16:P:198:ASP:N	16:P:206:ALA:HA	2.32	0.45
16:P:425:GLY:O	16:P:426:ALA:HB2	2.17	0.45
16:P:675:PHE:HZ	16:P:742:TRP:HZ3	1.61	0.45
1:A:474:LYS:HZ2	2:B:1096:SER:HB2	1.82	0.44
1:A:996:TYR:CE1	2:B:525:TRP:CE3	3.05	0.44
1:A:1154:LEU:O	1:A:1158:SER:HB2	2.17	0.44
1:A:1297:PHE:CD2	9:I:60:LEU:HD22	2.51	0.44
1:A:1574:ALA:HB3	9:I:122:ARG:HB3	1.99	0.44
1:A:1655:ASP:O	6:F:134:ILE:HA	2.17	0.44
2:B:78:PRO:O	2:B:79:LEU:HB3	2.17	0.44
16:P:366:PHE:HZ	16:P:433:VAL:HG12	1.82	0.44
16:P:435:ARG:NH2	18:R:140:ILE:CD1	2.80	0.44
16:P:533:LEU:H	16:P:554:ASN:HB2	1.82	0.44
18:R:299:THR:CG2	18:R:305:THR:HA	2.46	0.44
1:A:408:LYS:HG3	1:A:416:ARG:HE	1.72	0.44
1:A:1291:VAL:HG22	1:A:1473:LYS:HG3	1.98	0.44
2:B:923:GLN:HG2	2:B:949:ILE:CD1	2.47	0.44
2:B:1153:ILE:HA	2:B:1153:ILE:HD13	1.79	0.44
13:M:26:PHE:CE1	13:M:98:SER:HB2	2.51	0.44
17:Q:484:ALA:O	17:Q:488:LEU:HG	2.17	0.44
17:Q:494:SER:HB2	17:Q:497:GLN:H	1.82	0.44
18:R:236:PHE:CE2	18:R:253:ILE:HD12	2.52	0.44
1:A:257:ASN:OD1	1:A:258:GLU:N	2.51	0.44
1:A:507:TYR:CE1	1:A:508:PRO:C	2.87	0.44
1:A:1055:ILE:CD1	1:A:1178:LEU:HD23	2.44	0.44
2:B:107:PRO:HG2	2:B:133:TYR:CZ	2.52	0.44
2:B:143:TRP:CE3	2:B:446:MET:HE3	2.52	0.44
2:B:143:TRP:CD2	2:B:446:MET:HE3	2.52	0.44
2:B:699:ILE:HG22	2:B:700:LEU:HD12	1.98	0.44
2:B:833:PRO:HG2	2:B:836:TRP:CZ2	2.52	0.44
16:P:62:LYS:HE2	16:P:550:TYR:OH	2.17	0.44
16:P:198:ASP:HB2	16:P:206:ALA:HA	1.99	0.44
16:P:210:THR:HB	16:P:226:HIS:NE2	2.32	0.44
17:Q:374:THR:O	17:Q:377:PHE:HB3	2.17	0.44
1:A:535:GLN:HA	1:A:546:LEU:HG	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:920:PHE:CD1	1:A:921:PRO:HA	2.52	0.44
2:B:252:TYR:OH	2:B:305:ARG:NH1	2.44	0.44
2:B:1158:ILE:HA	2:B:1167:PHE:O	2.17	0.44
5:E:177:ARG:HD3	5:E:215:MET:HB2	2.00	0.44
15:O:506:PHE:CG	15:O:528:PHE:HZ	2.35	0.44
16:P:433:VAL:HG22	16:P:434:ARG:O	2.17	0.44
16:P:632:ILE:O	16:P:636:GLU:HG3	2.17	0.44
18:R:187:TYR:CE2	18:R:191:ILE:HG21	2.52	0.44
1:A:543:LEU:CA	17:Q:34:VAL:O	2.66	0.44
1:A:1260:LYS:HE2	1:A:1262:LEU:CG	2.47	0.44
2:B:42:VAL:HG21	2:B:190:ILE:HB	2.00	0.44
2:B:894:LYS:CG	12:L:47:ARG:HD2	2.47	0.44
16:P:290:GLU:HB3	16:P:342:GLN:HG2	1.99	0.44
16:P:532:GLU:HB2	16:P:554:ASN:CB	2.46	0.44
17:Q:221:PRO:HA	17:Q:225:GLN:HB2	1.99	0.44
17:Q:351:ASN:OD1	17:Q:369:TRP:CZ2	2.69	0.44
18:R:5:PRO:HD2	18:R:217:THR:HG21	1.94	0.44
18:R:217:THR:HG22	18:R:239:LEU:HD21	2.00	0.44
18:R:353:VAL:HG13	18:R:364:VAL:HB	1.98	0.44
1:A:1330:VAL:HG23	1:A:1455:ARG:HD2	2.00	0.44
2:B:1001:ALA:O	14:N:168:LEU:HD23	2.17	0.44
15:O:376:TYR:OH	15:O:377:TYR:CE2	2.66	0.44
15:O:515:ASN:N	15:O:516:PRO:HD3	2.33	0.44
16:P:323:ASN:HB3	16:P:350:THR:HB	1.98	0.44
17:Q:137:TRP:HE3	17:Q:140:ILE:HD11	1.82	0.44
18:R:317:LEU:HD13	18:R:367:ILE:HD11	2.00	0.44
1:A:477:ASN:C	2:B:1049:THR:HA	2.38	0.44
1:A:863:ASN:HB2	9:I:66:VAL:O	2.17	0.44
1:A:1248:ASP:OD1	1:A:1517:ARG:NH1	2.49	0.44
1:A:1323:HIS:HE1	1:A:1453:HIS:HB3	1.81	0.44
1:A:1575:ILE:CD1	9:I:122:ARG:CZ	2.95	0.44
1:A:1596:LEU:HD22	1:A:1602:GLY:HA2	2.00	0.44
2:B:548:LYS:HG2	2:B:695:ASN:O	2.18	0.44
2:B:894:LYS:CG	12:L:54:ARG:NH1	2.81	0.44
3:C:230:LEU:CD1	3:C:299:ILE:HD11	2.44	0.44
11:K:80:ILE:HD13	11:K:105:ILE:HD11	1.98	0.44
13:M:102:SER:HB3	13:M:105:SER:HB3	0.45	0.44
15:O:200:ASN:CB	17:Q:14:ASN:O	2.65	0.44
16:P:362:ARG:NH2	16:P:364:GLU:HG3	2.31	0.44
16:P:434:ARG:C	18:R:143:THR:OG1	2.47	0.44
16:P:472:ARG:N	16:P:504:THR:HG21	2.33	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:530:TRP:CZ2	1:A:607:VAL:HG21	2.53	0.44
1:A:581:ILE:HD11	1:A:585:ASP:CB	2.48	0.44
1:A:697:TYR:OH	11:K:102:ASN:HB3	2.17	0.44
1:A:721:LYS:HD2	8:H:90:ALA:HB1	2.00	0.44
1:A:912:VAL:HA	1:A:913:PRO:HA	1.84	0.44
2:B:535:ASP:OD1	2:B:720:GLN:NE2	2.49	0.44
2:B:623:ASP:OD2	2:B:648:ARG:NH2	2.40	0.44
2:B:1090:ASP:O	2:B:1094:ASN:CB	2.64	0.44
14:N:94:ASP:HB3	14:N:99:LEU:HG	2.00	0.44
16:P:274:ILE:HD13	16:P:305:PHE:CZ	2.53	0.44
16:P:331:LYS:HA	16:P:331:LYS:HD3	1.72	0.44
16:P:399:TRP:O	16:P:419:ARG:NH2	2.51	0.44
16:P:656:HIS:CD2	16:P:656:HIS:N	2.79	0.44
18:R:76:LYS:O	18:R:80:ARG:HG3	2.17	0.44
1:A:1275:THR:C	9:I:45:LEU:O	2.48	0.44
15:O:243:GLU:OE1	15:O:243:GLU:HA	2.17	0.44
16:P:574:TRP:HB3	16:P:578:PHE:CE2	2.53	0.44
17:Q:128:GLU:O	17:Q:132:VAL:HG23	2.17	0.44
1:A:37:VAL:HG12	1:A:38:LEU:HG	2.00	0.43
1:A:697:TYR:CD2	11:K:92:SER:HB3	2.53	0.43
1:A:1575:ILE:CG1	9:I:122:ARG:CZ	2.58	0.43
3:C:252:PRO:HD2	3:C:255:VAL:HG21	1.99	0.43
3:C:326:GLU:HB2	11:K:125:MET:HE3	1.98	0.43
7:G:163:PRO:HG2	7:G:166:TRP:CD1	2.52	0.43
16:P:229:ARG:HG3	16:P:231:ASN:H	1.82	0.43
16:P:363:ILE:HG23	16:P:374:VAL:HG13	2.00	0.43
17:Q:140:ILE:HG22	17:Q:236:MET:HG2	2.00	0.43
18:R:19:LEU:HB3	18:R:188:PHE:CD1	2.52	0.43
18:R:75:GLN:HA	18:R:78:ARG:NE	2.32	0.43
18:R:80:ARG:O	18:R:83:HIS:HB3	2.18	0.43
18:R:138:PHE:CE1	18:R:140:ILE:HD11	2.53	0.43
1:A:403:LEU:HD12	1:A:403:LEU:HA	1.71	0.43
1:A:472:MET:HG3	2:B:1073:GLU:CD	2.34	0.43
1:A:1003:ARG:HH22	2:B:530:PRO:HA	1.84	0.43
1:A:1025:LYS:HZ2	2:B:1076:ARG:NH1	2.16	0.43
1:A:1053:ASP:C	1:A:1055:ILE:HG12	2.36	0.43
15:O:189:PHE:HA	15:O:192:THR:HG23	2.00	0.43
15:O:581:THR:HA	15:O:584:GLN:CD	2.38	0.43
16:P:21:GLN:HB2	18:R:139:GLU:CD	2.38	0.43
16:P:194:ARG:HG2	16:P:209:LYS:O	2.18	0.43
16:P:238:LEU:HD22	16:P:284:VAL:H	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:P:363:ILE:O	16:P:363:ILE:HD12	2.18	0.43
16:P:413:GLY:HA2	16:P:426:ALA:HB2	1.99	0.43
16:P:428:GLU:HB3	18:R:142:ARG:HH11	1.81	0.43
16:P:584:ARG:O	16:P:588:SER:CB	2.62	0.43
16:P:751:SER:O	16:P:753:PHE:N	2.51	0.43
17:Q:355:VAL:HG12	18:R:212:HIS:ND1	2.32	0.43
18:R:4:VAL:HG22	18:R:214:VAL:HA	1.99	0.43
18:R:186:LEU:C	18:R:186:LEU:CD1	2.86	0.43
18:R:299:THR:HG21	18:R:305:THR:HA	2.00	0.43
1:A:414:GLU:O	1:A:416:ARG:N	2.52	0.43
1:A:475:ARG:O	2:B:1059:PRO:CG	2.66	0.43
1:A:478:TYR:CZ	2:B:1049:THR:HB	2.53	0.43
1:A:684:ASP:OD2	8:H:20:TYR:CA	2.66	0.43
2:B:26:ILE:HD11	10:J:58:GLU:HG2	2.00	0.43
2:B:212:ASN:CG	2:B:361:HIS:CG	2.92	0.43
3:C:292:GLY:CA	3:C:295:ARG:NH2	2.80	0.43
7:G:159:LYS:HD2	15:O:103:ASN:ND2	2.28	0.43
15:O:198:PHE:CD2	15:O:199:PRO:HD2	2.53	0.43
15:O:224:GLU:H	15:O:224:GLU:CD	2.17	0.43
16:P:257:ARG:HG3	16:P:411:LYS:HZ3	1.83	0.43
16:P:361:LYS:HA	16:P:375:PHE:O	2.18	0.43
16:P:369:PHE:O	16:P:369:PHE:HD1	2.01	0.43
16:P:394:VAL:HG11	18:R:144:VAL:HG21	1.95	0.43
16:P:686:TYR:O	16:P:691:VAL:HG11	2.17	0.43
17:Q:19:LEU:CD1	17:Q:27:ARG:CB	2.94	0.43
17:Q:137:TRP:CE3	17:Q:140:ILE:HD11	2.53	0.43
17:Q:502:ILE:HA	17:Q:505:ILE:HG22	1.99	0.43
1:A:545:SER:OG	17:Q:26:ARG:NH2	2.50	0.43
1:A:581:ILE:CG1	1:A:585:ASP:OD2	2.56	0.43
1:A:629:ASP:O	2:B:916:LYS:HE2	2.17	0.43
1:A:862:THR:HG22	9:I:67:VAL:HG12	1.81	0.43
2:B:1092:LEU:C	2:B:1096:SER:HB2	2.37	0.43
6:F:70:LYS:HA	7:G:94:PRO:HG3	1.83	0.43
7:G:24:VAL:N	7:G:128:GLN:CD	2.28	0.43
15:O:56:VAL:CG2	15:O:99:ILE:HD12	2.48	0.43
15:O:200:ASN:HB2	17:Q:14:ASN:HB3	1.70	0.43
16:P:319:ASP:HB2	16:P:363:ILE:CG1	2.48	0.43
16:P:507:GLY:O	16:P:539:VAL:HA	2.19	0.43
16:P:705:HIS:ND1	20:P:902:SO4:O4	2.51	0.43
17:Q:106:LYS:O	17:Q:110:PHE:HB3	2.18	0.43
18:R:18:LYS:HA	18:R:78:ARG:HD3	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:R:76:LYS:HA	18:R:79:ARG:HB2	2.01	0.43
18:R:348:LYS:HE2	18:R:352:TRP:HE1	1.83	0.43
1:A:36:THR:HG22	1:A:45:VAL:HG21	2.00	0.43
1:A:407:GLN:HB3	1:A:409:ASP:N	2.23	0.43
1:A:477:ASN:CB	2:B:1047:ARG:NH1	2.81	0.43
2:B:209:GLN:CG	2:B:210:ARG:H	2.08	0.43
3:C:253:PRO:N	14:N:180:PHE:CB	2.72	0.43
7:G:24:VAL:CA	7:G:25:THR:HA	2.32	0.43
15:O:376:TYR:CD1	15:O:376:TYR:O	2.70	0.43
16:P:474:LYS:CD	16:P:474:LYS:H	2.30	0.43
16:P:487:ASN:O	18:R:138:PHE:CZ	2.67	0.43
16:P:730:GLU:O	16:P:734:LYS:HB2	2.19	0.43
17:Q:234:CYS:SG	17:Q:284:LEU:HB3	2.57	0.43
1:A:507:TYR:CD1	1:A:508:PRO:O	2.65	0.43
1:A:677:GLY:HA3	1:A:786:TYR:OH	2.18	0.43
1:A:921:PRO:CD	8:H:19:ARG:HG3	2.42	0.43
1:A:1484:LEU:HD22	2:B:305:ARG:NH2	2.34	0.43
2:B:46:ILE:HG13	2:B:192:GLY:HA2	1.99	0.43
2:B:57:ASP:OD1	2:B:57:ASP:N	2.52	0.43
16:P:397:LYS:NZ	18:R:85:ARG:HG2	2.31	0.43
16:P:412:ASN:O	16:P:426:ALA:HB1	2.18	0.43
18:R:5:PRO:CD	18:R:217:THR:HB	2.16	0.43
1:A:486:PRO:CG	2:B:781:TYR:O	2.67	0.43
1:A:1269:LYS:HB2	1:A:1269:LYS:HE3	1.89	0.43
1:A:1463:ASP:HB2	1:A:1469:TRP:CE2	2.52	0.43
2:B:30:LYS:HG2	2:B:178:TYR:HB2	2.00	0.43
2:B:75:ASP:HA	2:B:440:PHE:CZ	2.53	0.43
2:B:954:PHE:H	2:B:955:PRO:HD2	1.83	0.43
7:G:143:SER:CB	15:O:104:ILE:HB	2.48	0.43
12:L:32:ALA:HB3	12:L:55:ILE:HG23	2.01	0.43
16:P:438:TRP:HD1	18:R:141:TRP:CH2	2.35	0.43
16:P:472:ARG:CD	18:R:200:THR:CG2	2.96	0.43
17:Q:366:TYR:CD1	18:R:215:THR:HG23	2.53	0.43
17:Q:369:TRP:CA	17:Q:373:GLU:OE2	2.66	0.43
1:A:475:ARG:CD	2:B:1059:PRO:O	2.67	0.43
9:I:26:SER:O	9:I:39:LYS:HB2	2.19	0.43
15:O:76:ASN:O	15:O:80:LEU:HD13	2.18	0.43
15:O:444:SER:O	15:O:448:SER:HB3	2.18	0.43
15:O:473:PHE:HZ	15:O:509:MET:HE3	1.84	0.43
16:P:187:ILE:HG22	18:R:195:LEU:HD23	1.98	0.43
16:P:361:LYS:HG3	16:P:376:ASP:HB3	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:P:697:GLU:HG2	16:P:698:LYS:H	1.84	0.43
16:P:760:ILE:O	16:P:764:LEU:HG	2.18	0.43
17:Q:105:LEU:HD13	17:Q:141:LEU:HD11	1.99	0.43
17:Q:239:PHE:CG	17:Q:240:LYS:N	2.86	0.43
17:Q:255:LYS:O	17:Q:259:GLN:HB2	2.18	0.43
18:R:180:CYS:SG	18:R:185:LYS:HG3	2.59	0.43
1:A:827:THR:HG21	1:A:924:SER:CB	2.49	0.43
1:A:828:CYS:HG	2:B:1027:TYR:CB	2.30	0.43
1:A:909:SER:CA	9:I:83:LYS:HZ3	2.26	0.43
1:A:991:LYS:CB	1:A:994:GLU:HG3	2.48	0.43
1:A:1313:LEU:O	1:A:1317:ILE:HD12	2.18	0.43
1:A:1484:LEU:HB3	2:B:305:ARG:NH2	2.34	0.43
1:A:1604:GLU:CD	1:A:1621:PHE:HE1	2.21	0.43
2:B:551:ILE:CG2	2:B:648:ARG:H	2.22	0.43
15:O:48:SER:O	15:O:49:ALA:C	2.57	0.43
15:O:107:ILE:O	15:O:109:SER:N	2.47	0.43
15:O:218:LEU:HD12	15:O:221:TYR:CZ	2.54	0.43
15:O:376:TYR:CG	15:O:376:TYR:O	2.70	0.43
17:Q:4:PHE:HE1	17:Q:18:ARG:HH11	1.67	0.43
17:Q:160:SER:HA	17:Q:163:SER:HB2	2.00	0.43
17:Q:366:TYR:CE1	18:R:215:THR:HG23	2.54	0.43
17:Q:375:LEU:HD23	17:Q:375:LEU:HA	1.88	0.43
17:Q:378:LEU:HD22	18:R:235:ILE:HA	2.01	0.43
17:Q:406:GLN:HA	17:Q:409:ALA:HB3	2.00	0.43
18:R:25:ASN:O	18:R:29:ARG:HB2	2.19	0.43
1:A:697:TYR:CE2	11:K:92:SER:CB	3.01	0.43
2:B:681:ILE:HB	14:N:154:ARG:HB2	2.01	0.43
2:B:848:ILE:N	12:L:60:ARG:NE	2.67	0.43
3:C:222:VAL:C	3:C:224:THR:H	2.20	0.43
15:O:175:MET:HE2	15:O:175:MET:HA	2.00	0.43
15:O:202:ASN:OD1	15:O:202:ASN:N	2.52	0.43
16:P:193:LEU:HD12	16:P:251:SER:N	2.31	0.43
17:Q:132:VAL:O	17:Q:136:ILE:HG13	2.19	0.43
1:A:629:ASP:CA	2:B:926:VAL:HG23	2.46	0.42
2:B:48:SER:HB3	2:B:404:LEU:CD1	2.49	0.42
2:B:77:LYS:NZ	2:B:439:ASN:HA	2.33	0.42
2:B:345:SER:CA	13:M:113:ILE:HG12	2.48	0.42
7:G:29:ASP:OD1	7:G:30:GLU:N	2.52	0.42
7:G:35:SER:OG	7:G:132:VAL:N	2.46	0.42
9:I:34:LYS:HA	9:I:34:LYS:HD3	1.86	0.42
16:P:265:THR:HG21	16:P:303:VAL:HG21	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:P:472:ARG:NH1	18:R:203:SER:HB2	2.33	0.42
17:Q:177:TYR:OH	17:Q:252:LEU:N	2.52	0.42
18:R:248:LYS:O	18:R:250:LEU:N	2.49	0.42
1:A:489:ASN:HB3	11:K:95:HIS:CD2	2.54	0.42
1:A:1172:LEU:O	1:A:1176:ARG:HG2	2.19	0.42
2:B:45:HIS:CD2	2:B:500:PHE:HD1	2.37	0.42
2:B:49:PHE:HE2	2:B:194:PHE:CZ	2.30	0.42
2:B:550:ARG:H	2:B:650:LEU:H	1.66	0.42
2:B:893:ASN:O	2:B:895:PHE:HD1	2.01	0.42
13:M:8:SER:O	14:N:71:PRO:HA	2.19	0.42
15:O:66:ASN:CG	15:O:111:ARG:NH1	2.72	0.42
16:P:300:LEU:N	16:P:300:LEU:HD23	2.34	0.42
16:P:330:PRO:HG3	16:P:342:GLN:HG3	2.00	0.42
18:R:234:LYS:O	18:R:238:THR:OG1	2.33	0.42
1:A:4:SER:HB2	1:A:573:LEU:CD2	2.49	0.42
1:A:475:ARG:NH2	2:B:1061:LYS:HD2	2.34	0.42
1:A:722:PRO:HD2	8:H:95:TYR:HD1	1.83	0.42
1:A:1053:ASP:OD2	5:E:204:THR:CG2	2.67	0.42
1:A:1242:ILE:HG22	1:A:1536:ILE:HG22	2.01	0.42
2:B:527:PHE:CD1	2:B:666:PRO:CB	2.99	0.42
2:B:574:SER:HB3	13:M:67:ASP:OD2	2.20	0.42
2:B:809:VAL:HG13	2:B:901:VAL:HB	2.01	0.42
2:B:883:GLU:HG3	2:B:906:ARG:HB2	2.01	0.42
16:P:390:GLN:C	18:R:149:LYS:HB3	2.38	0.42
16:P:438:TRP:NE1	18:R:297:PHE:HZ	2.16	0.42
17:Q:6:ARG:HA	17:Q:18:ARG:CD	2.50	0.42
17:Q:410:ARG:HA	17:Q:413:LEU:CB	2.45	0.42
17:Q:495:LYS:HE2	17:Q:499:LYS:HZ1	1.85	0.42
18:R:361:ASP:C	18:R:363:GLU:N	2.73	0.42
1:A:476:VAL:O	2:B:1068:GLY:CA	2.47	0.42
1:A:953:GLU:CA	1:A:1205:PHE:CG	2.85	0.42
1:A:1313:LEU:CG	1:A:1462:PHE:CE1	2.73	0.42
1:A:1606:SER:HB3	1:A:1611:MET:HE3	2.02	0.42
1:A:1657:LEU:CB	7:G:104:LEU:HD22	2.47	0.42
2:B:243:GLN:CD	2:B:646:HIS:HE2	2.20	0.42
2:B:563:SER:CA	13:M:73:SER:HB3	2.48	0.42
14:N:81:THR:HG22	14:N:86:ASP:HB3	2.01	0.42
15:O:56:VAL:HG23	15:O:57:LYS:N	2.35	0.42
15:O:96:LEU:O	15:O:100:LEU:HG	2.20	0.42
15:O:379:ARG:NH1	15:O:382:GLN:HE22	2.17	0.42
15:O:468:GLU:HG2	15:O:469:ARG:N	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:P:473:HIS:CG	16:P:475:ARG:HD2	2.54	0.42
16:P:619:GLU:OE2	16:P:670:ALA:N	2.52	0.42
16:P:659:LEU:H	16:P:659:LEU:CD1	2.27	0.42
17:Q:258:MET:HB3	17:Q:258:MET:HE2	1.94	0.42
18:R:8:LEU:H	18:R:8:LEU:HD22	1.83	0.42
1:A:83:VAL:HG13	1:A:427:PHE:CZ	2.52	0.42
1:A:1325:LEU:HD21	1:A:1474:LEU:HD11	2.00	0.42
3:C:315:PHE:HE2	11:K:139:ILE:CD1	2.30	0.42
8:H:105:GLU:HG2	8:H:115:TYR:HE1	1.84	0.42
15:O:453:TYR:CE2	15:O:473:PHE:HB2	2.54	0.42
16:P:321:LYS:HD3	16:P:321:LYS:N	2.25	0.42
16:P:390:GLN:N	18:R:150:GLN:O	2.52	0.42
16:P:434:ARG:CG	18:R:143:THR:CB	2.90	0.42
16:P:675:PHE:HZ	16:P:742:TRP:CZ3	2.36	0.42
17:Q:262:LEU:HD23	17:Q:262:LEU:HA	1.84	0.42
17:Q:344:THR:HG22	17:Q:436:LEU:HD13	2.01	0.42
1:A:83:VAL:HG21	1:A:427:PHE:CZ	2.55	0.42
1:A:410:LYS:HB3	1:A:411:VAL:CG2	2.50	0.42
1:A:474:LYS:HZ2	2:B:1092:LEU:CD2	2.08	0.42
1:A:826:PHE:CG	1:A:827:THR:N	2.88	0.42
1:A:878:ARG:HH11	9:I:66:VAL:HG21	1.63	0.42
1:A:1085:LEU:HD22	6:F:84:TYR:HH	1.81	0.42
1:A:1263:LEU:HD12	1:A:1498:ILE:HD11	2.02	0.42
2:B:146:ASN:HD22	2:B:441:LYS:HZ1	1.67	0.42
2:B:682:GLN:HA	14:N:154:ARG:CZ	2.46	0.42
2:B:799:GLY:O	2:B:911:PRO:HG3	2.20	0.42
3:C:61:THR:HA	3:C:298:PHE:CZ	2.55	0.42
3:C:71:MET:HE3	3:C:313:ILE:HG22	2.02	0.42
3:C:274:THR:HG21	14:N:171:PHE:HA	1.60	0.42
14:N:63:ASP:OD2	14:N:66:LYS:NZ	2.35	0.42
15:O:199:PRO:HD3	15:O:211:TYR:CG	2.54	0.42
16:P:273:ARG:NH1	16:P:288:SER:OG	2.53	0.42
16:P:607:VAL:HB	16:P:731:LEU:HD13	2.01	0.42
18:R:253:ILE:HG12	18:R:257:ILE:HG13	2.02	0.42
1:A:410:LYS:HB2	1:A:411:VAL:HG23	2.01	0.42
1:A:436:ALA:O	1:A:440:SER:HA	2.15	0.42
1:A:475:ARG:NH2	2:B:1061:LYS:CD	2.82	0.42
1:A:564:PRO:CD	15:O:370:THR:O	2.68	0.42
1:A:711:LYS:HA	11:K:104:ARG:NH2	2.35	0.42
1:A:909:SER:HA	9:I:83:LYS:HZ1	1.76	0.42
1:A:1063:MET:HE1	1:A:1174:TYR:CD2	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1657:LEU:O	6:F:132:LEU:CA	2.68	0.42
3:C:116:VAL:HG11	3:C:125:LYS:HE3	2.01	0.42
3:C:170:GLU:HA	3:C:171:PRO:HD3	1.84	0.42
7:G:160:ASN:OD1	7:G:160:ASN:N	2.52	0.42
13:M:101:VAL:CG1	13:M:105:SER:OG	2.66	0.42
15:O:234:ILE:HA	15:O:234:ILE:HD13	1.74	0.42
16:P:366:PHE:CZ	16:P:433:VAL:HG12	2.54	0.42
16:P:427:SER:HB2	16:P:429:SER:O	2.19	0.42
16:P:648:SER:HA	16:P:757:GLN:NE2	2.35	0.42
17:Q:120:ILE:HA	17:Q:125:PHE:HB2	2.01	0.42
17:Q:351:ASN:O	17:Q:355:VAL:HG23	2.19	0.42
1:A:407:GLN:C	1:A:409:ASP:H	2.23	0.42
2:B:897:GLU:HA	12:L:46:VAL:HG21	2.01	0.42
3:C:105:PRO:HG3	10:J:6:ARG:CZ	2.50	0.42
4:D:82:LEU:O	4:D:86:ILE:HG23	2.20	0.42
15:O:364:LEU:HB3	15:O:385:MET:HE3	2.01	0.42
15:O:376:TYR:CG	15:O:419:LYS:CD	3.03	0.42
15:O:400:LEU:O	15:O:404:ILE:HG13	2.19	0.42
16:P:187:ILE:HG23	18:R:195:LEU:CD2	2.50	0.42
16:P:443:ASP:O	18:R:3:GLU:CA	2.66	0.42
16:P:663:LEU:HD12	16:P:664:GLU:N	2.34	0.42
1:A:990:ILE:CA	1:A:994:GLU:OE1	2.26	0.42
2:B:656:LEU:HD21	2:B:689:VAL:HG12	2.02	0.42
2:B:697:LEU:HD13	2:B:702:ASN:HA	2.02	0.42
11:K:93:ILE:HA	11:K:94:PRO:HD2	1.75	0.42
15:O:77:GLN:HG2	15:O:88:ILE:HB	2.01	0.42
15:O:236:LYS:HD3	15:O:236:LYS:HA	1.73	0.42
16:P:350:THR:HG23	18:R:153:ASN:CG	2.40	0.42
16:P:465:VAL:HG13	16:P:480:VAL:HG13	2.01	0.42
17:Q:152:LEU:HA	17:Q:152:LEU:HD13	1.67	0.42
17:Q:257:VAL:HG13	17:Q:262:LEU:HB2	2.02	0.42
17:Q:502:ILE:O	17:Q:506:LYS:HB2	2.20	0.42
1:A:227:LEU:HD23	1:A:227:LEU:HA	1.84	0.42
1:A:407:GLN:C	1:A:408:LYS:NZ	2.73	0.42
1:A:498:PRO:HA	1:A:499:PRO:HD3	1.81	0.42
1:A:550:SER:OG	1:A:553:GLN:HG3	2.19	0.42
1:A:692:TYR:O	1:A:696:ILE:HG12	2.19	0.42
1:A:874:GLU:OE2	1:A:878:ARG:HD2	2.20	0.42
1:A:1318:SER:HA	1:A:1450:ILE:HD13	2.00	0.42
2:B:196:VAL:HG21	2:B:465:LEU:HB3	2.02	0.42
2:B:394:PRO:O	2:B:400:GLN:NE2	2.48	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:230:LEU:O	3:C:293:ARG:HA	2.20	0.42
15:O:66:ASN:ND2	15:O:111:ARG:CZ	2.83	0.42
15:O:175:MET:HE3	15:O:175:MET:HB2	1.91	0.42
16:P:368:HIS:HB3	16:P:411:LYS:NZ	2.34	0.42
17:Q:103:LEU:HD21	17:Q:205:ILE:HD13	2.00	0.42
17:Q:409:ALA:O	17:Q:413:LEU:CB	2.58	0.42
1:A:407:GLN:O	1:A:408:LYS:HE2	2.19	0.41
1:A:1260:LYS:HE2	1:A:1262:LEU:HD21	2.01	0.41
1:A:1314:GLN:CD	1:A:1446:ARG:HH11	2.13	0.41
2:B:800:TYR:OH	2:B:908:ARG:CZ	2.65	0.41
16:P:484:ARG:HB2	16:P:488:LEU:HB3	2.02	0.41
17:Q:498:LEU:O	17:Q:502:ILE:HG23	2.20	0.41
18:R:150:GLN:H	18:R:150:GLN:HG2	1.26	0.41
1:A:82:PRO:HD3	1:A:393:SER:OG	2.20	0.41
1:A:474:LYS:CE	2:B:1096:SER:OG	2.63	0.41
1:A:581:ILE:CG1	1:A:582:LYS:N	2.83	0.41
2:B:145:VAL:HG21	2:B:440:PHE:O	2.20	0.41
2:B:1005:TYR:CE2	14:N:170:HIS:CE1	3.08	0.41
3:C:314:PHE:HD2	11:K:135:PHE:CE2	2.38	0.41
5:E:67:GLU:CD	5:E:67:GLU:H	2.23	0.41
15:O:548:ASN:O	15:O:552:LEU:HG	2.21	0.41
16:P:64:LEU:CD2	16:P:64:LEU:H	2.33	0.41
16:P:350:THR:CG2	18:R:153:ASN:CG	2.88	0.41
16:P:535:VAL:HG13	16:P:552:LEU:HD12	2.01	0.41
16:P:740:ILE:O	16:P:744:LEU:HG	2.19	0.41
16:P:762:ARG:HG3	17:Q:139:LYS:NZ	2.35	0.41
17:Q:192:TYR:CD1	17:Q:193:PHE:CD1	3.08	0.41
17:Q:282:ARG:HG2	17:Q:302:ALA:HB1	2.02	0.41
17:Q:329:LYS:O	17:Q:332:LEU:N	2.53	0.41
17:Q:341:ARG:NH1	17:Q:369:TRP:CD1	2.87	0.41
18:R:158:THR:OG1	18:R:159:TYR:N	2.53	0.41
18:R:220:LEU:N	18:R:235:ILE:HG21	2.36	0.41
18:R:312:TYR:HA	18:R:315:SER:HG	1.85	0.41
18:R:421:LYS:HG3	18:R:422:GLY:N	2.34	0.41
1:A:451:VAL:HA	1:A:452:PRO:HD3	1.95	0.41
1:A:501:PHE:CD1	2:B:1046:VAL:HG21	2.55	0.41
1:A:986:PHE:CD2	2:B:958:MET:CE	3.03	0.41
1:A:1025:LYS:HZ1	2:B:1076:ARG:NH1	2.18	0.41
1:A:1180:ASN:N	1:A:1180:ASN:HD22	2.18	0.41
1:A:1538:VAL:HG21	5:E:142:VAL:HG22	2.01	0.41
2:B:1151:ILE:HG23	7:G:21:LYS:CG	2.47	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:O:78:VAL:HA	15:O:88:ILE:HG22	2.00	0.41
16:P:263:ILE:HB	16:P:275:GLU:O	2.21	0.41
16:P:397:LYS:CD	18:R:85:ARG:HD3	2.49	0.41
16:P:489:PHE:CD2	18:R:140:ILE:HD11	2.48	0.41
16:P:607:VAL:O	16:P:611:ILE:HG13	2.21	0.41
17:Q:287:TRP:HE1	17:Q:289:ARG:HB3	1.86	0.41
18:R:6:ILE:HG21	18:R:210:THR:HG22	2.02	0.41
18:R:268:LEU:HD11	18:R:316:SER:OG	2.20	0.41
2:B:49:PHE:HB3	2:B:164:MET:SD	2.60	0.41
2:B:61:LEU:HA	2:B:61:LEU:HD23	1.75	0.41
2:B:401:GLU:C	2:B:402:VAL:HG23	2.41	0.41
2:B:995:TYR:HE1	14:N:162:LYS:HA	1.85	0.41
15:O:219:ARG:CZ	15:O:360:VAL:CG2	2.98	0.41
15:O:235:GLU:HA	15:O:237:ILE:HB	2.01	0.41
15:O:244:LEU:HD23	15:O:244:LEU:O	2.20	0.41
16:P:378:SER:HB2	16:P:379:LYS:HD2	2.03	0.41
16:P:454:GLN:HB3	16:P:465:VAL:HG23	2.02	0.41
17:Q:6:ARG:HA	17:Q:18:ARG:HG3	2.02	0.41
18:R:209:ARG:H	18:R:209:ARG:HD3	1.85	0.41
18:R:436:LYS:HA	18:R:439:GLU:HB2	2.02	0.41
1:A:711:LYS:HA	11:K:104:ARG:HH22	1.84	0.41
1:A:826:PHE:HE1	2:B:952:HIS:CE1	2.39	0.41
1:A:878:ARG:HG2	9:I:66:VAL:CG2	2.23	0.41
1:A:1622:LEU:HD21	2:B:1189:LEU:HD22	2.01	0.41
2:B:1005:TYR:CZ	14:N:170:HIS:NE2	2.87	0.41
3:C:246:ARG:HD2	3:C:284:GLU:OE2	2.21	0.41
11:K:95:HIS:HB3	11:K:98:GLU:HG2	2.03	0.41
15:O:169:THR:O	15:O:172:HIS:N	2.52	0.41
16:P:389:TRP:CZ2	18:R:147:GLN:CA	2.95	0.41
17:Q:15:CYS:CB	17:Q:17:SER:H	2.30	0.41
17:Q:26:ARG:CB	17:Q:34:VAL:HG11	2.43	0.41
17:Q:318:LEU:HD12	17:Q:318:LEU:HA	1.78	0.41
17:Q:355:VAL:CG1	18:R:212:HIS:ND1	2.83	0.41
1:A:68:ASP:C	1:A:70:LYS:H	2.24	0.41
1:A:481:ARG:N	2:B:1045:GLN:O	2.53	0.41
1:A:506:THR:HG22	1:A:580:HIS:N	2.31	0.41
1:A:507:TYR:CD1	1:A:509:GLU:N	2.89	0.41
1:A:1055:ILE:HD13	1:A:1178:LEU:CD2	2.48	0.41
1:A:1484:LEU:HD23	2:B:304:ASP:HB2	2.01	0.41
1:A:1573:TYR:HA	9:I:111:PHE:CE2	2.55	0.41
2:B:550:ARG:HA	2:B:550:ARG:HD3	1.81	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:679:GLN:NE2	14:N:156:PRO:O	2.53	0.41
12:L:33:GLU:HG3	12:L:53:HIS:ND1	2.36	0.41
15:O:129:PRO:O	15:O:130:PRO:C	2.59	0.41
15:O:372:VAL:HG22	15:O:381:ILE:HD13	2.03	0.41
16:P:65:LEU:HD21	16:P:226:HIS:CE1	2.55	0.41
16:P:347:LEU:HD12	16:P:347:LEU:N	2.35	0.41
17:Q:156:LEU:HD23	17:Q:156:LEU:HA	1.84	0.41
18:R:19:LEU:HB3	18:R:188:PHE:HD1	1.86	0.41
18:R:362:ALA:CB	18:R:421:LYS:HB3	2.38	0.41
1:A:514:TYR:CE1	6:F:115:THR:O	2.74	0.41
1:A:721:LYS:HZ2	8:H:91:ASP:HA	1.80	0.41
1:A:938:VAL:HG22	9:I:82:ILE:HD11	1.93	0.41
2:B:186:GLU:OE2	2:B:731:VAL:HB	2.20	0.41
2:B:469:ASN:OD1	2:B:482:SER:CB	2.67	0.41
4:D:37:LEU:HD23	4:D:37:LEU:HA	1.88	0.41
14:N:25:ILE:HA	14:N:26:PRO:HD3	1.84	0.41
16:P:448:THR:HG21	16:P:471:MET:HB2	2.03	0.41
17:Q:26:ARG:H	17:Q:26:ARG:HG3	1.57	0.41
17:Q:136:ILE:HG12	17:Q:243:PHE:CZ	2.56	0.41
18:R:219:LEU:HD23	18:R:219:LEU:HA	1.83	0.41
1:A:407:GLN:C	1:A:409:ASP:N	2.74	0.41
1:A:413:LEU:HD13	1:A:416:ARG:HG3	2.03	0.41
1:A:684:ASP:OD2	8:H:21:ASN:N	2.51	0.41
1:A:1329:ILE:HB	1:A:1456:PHE:CE2	2.41	0.41
11:K:50:LEU:O	11:K:54:THR:HG23	2.20	0.41
16:P:304:ASP:HB2	16:P:363:ILE:O	2.20	0.41
16:P:458:LYS:HD3	16:P:461:HIS:CE1	2.46	0.41
16:P:577:LEU:O	17:Q:506:LYS:NZ	2.47	0.41
16:P:712:ASP:O	16:P:715:TYR:N	2.53	0.41
16:P:762:ARG:NE	16:P:762:ARG:HA	2.34	0.41
17:Q:109:GLN:CD	17:Q:137:TRP:HE1	2.24	0.41
17:Q:188:ALA:C	17:Q:384:GLN:CG	2.89	0.41
1:A:67:LEU:HB2	1:A:72:CYS:HB2	2.02	0.41
1:A:315:ILE:HG13	1:A:319:GLU:HB2	2.03	0.41
1:A:382:GLN:HE21	1:A:456:VAL:CG2	2.28	0.41
1:A:406:LEU:CB	1:A:408:LYS:H	2.29	0.41
1:A:634:ASN:OD1	2:B:1069:ILE:HG12	2.21	0.41
1:A:1000:MET:HG2	2:B:520:LEU:HD23	2.02	0.41
1:A:1025:LYS:HD2	1:A:1025:LYS:HA	1.85	0.41
1:A:1195:GLU:HB3	1:A:1196:PRO:HD3	2.03	0.41
1:A:1603:MET:HE1	1:A:1615:TYR:HD2	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:149:GLU:OE1	2:B:441:LYS:HE2	2.15	0.41
2:B:262:PHE:CE1	2:B:357:ILE:HD13	2.56	0.41
2:B:279:ALA:HB2	2:B:326:VAL:HG12	2.03	0.41
3:C:58:ASN:C	3:C:296:ASN:ND2	2.72	0.41
3:C:314:PHE:HE2	11:K:135:PHE:CD1	2.39	0.41
7:G:50:ALA:HA	7:G:113:PHE:CD2	2.56	0.41
7:G:144:HIS:NE2	15:O:145:SER:CA	2.84	0.41
7:G:159:LYS:HB3	15:O:105:ASN:ND2	2.12	0.41
11:K:54:THR:HG22	11:K:62:SER:H	1.86	0.41
15:O:232:LEU:HD12	15:O:232:LEU:HA	1.74	0.41
15:O:430:ARG:NH2	15:O:596:PRO:HD3	2.36	0.41
15:O:592:PHE:HA	15:O:593:PRO:HD3	1.90	0.41
16:P:56:ASP:HB2	16:P:554:ASN:OD1	2.21	0.41
16:P:408:ILE:HG23	16:P:413:GLY:C	2.41	0.41
16:P:432:PRO:HB2	18:R:146:SER:CB	2.49	0.41
16:P:475:ARG:HG2	18:R:1:MET:HE2	1.26	0.41
16:P:596:ILE:HD13	17:Q:272:GLN:OE1	2.20	0.41
17:Q:26:ARG:HD2	17:Q:34:VAL:HG11	2.02	0.41
17:Q:375:LEU:HA	17:Q:378:LEU:HD12	2.01	0.41
17:Q:509:CYS:O	17:Q:513:MET:HB2	2.20	0.41
18:R:15:GLN:O	18:R:18:LYS:HB2	2.21	0.41
18:R:173:MET:O	18:R:176:PRO:HD2	2.20	0.41
18:R:430:LEU:O	18:R:434:GLN:HG3	2.21	0.41
1:A:436:ALA:N	1:A:439:ASP:O	2.54	0.41
1:A:680:LEU:O	1:A:728:GLY:HA3	2.20	0.41
1:A:703:GLU:HG2	11:K:50:LEU:HD13	2.02	0.41
1:A:1317:ILE:O	1:A:1322:ILE:HG12	2.21	0.41
1:A:1600:ARG:NH2	1:A:1617:THR:HG1	2.10	0.41
2:B:152:LEU:HA	2:B:443:LYS:HE3	1.94	0.41
2:B:206:LEU:O	2:B:402:VAL:HG13	2.21	0.41
3:C:236:LEU:HD11	3:C:290:LYS:HG3	2.02	0.41
9:I:87:PRO:HG2	9:I:119:TYR:CE2	2.56	0.41
16:P:317:ILE:CG1	16:P:326:ILE:HD13	2.49	0.41
17:Q:140:ILE:O	17:Q:143:THR:HG22	2.21	0.41
17:Q:178:THR:HG21	17:Q:227:TYR:OH	2.21	0.41
17:Q:245:SER:HB3	17:Q:284:LEU:HD13	2.03	0.41
17:Q:408:ILE:HD11	17:Q:412:LYS:HE3	2.02	0.41
18:R:303:THR:HA	18:R:358:PHE:HZ	1.85	0.41
1:A:385:LEU:HA	1:A:385:LEU:HD23	1.88	0.40
1:A:413:LEU:HD22	1:A:413:LEU:HA	1.78	0.40
1:A:1056:ASP:OD2	1:A:1057:ILE:N	2.54	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1326:GLU:HB3	1:A:1455:ARG:NH1	2.36	0.40
2:B:527:PHE:CG	2:B:666:PRO:HG3	2.34	0.40
2:B:1002:LYS:O	14:N:168:LEU:HD23	2.21	0.40
7:G:166:TRP:HZ3	7:G:225:ILE:HD13	1.87	0.40
8:H:95:TYR:HD2	8:H:144:ILE:HD12	1.86	0.40
15:O:115:LEU:O	15:O:119:ILE:HG13	2.21	0.40
15:O:124:LYS:O	15:O:127:GLU:HB2	2.22	0.40
15:O:383:TYR:CE2	15:O:597:LEU:HD13	2.56	0.40
16:P:389:TRP:CZ2	18:R:149:LYS:N	2.79	0.40
16:P:500:ILE:HB	16:P:501:PRO:CD	2.51	0.40
18:R:408:ILE:HG23	18:R:435:LEU:HD13	2.03	0.40
1:A:394:LEU:HD23	1:A:394:LEU:HA	1.86	0.40
1:A:487:ASP:HB2	1:A:615:ARG:HB3	2.02	0.40
1:A:615:ARG:NH1	2:B:929:ARG:CD	2.82	0.40
1:A:741:PRO:HA	1:A:742:PRO:HD3	1.68	0.40
1:A:1024:THR:HG22	1:A:1190:SER:CB	2.50	0.40
1:A:1613:MET:HG2	1:A:1618:THR:HG23	2.03	0.40
2:B:152:LEU:CD2	2:B:443:LYS:HE3	2.51	0.40
2:B:551:ILE:CG2	2:B:647:SER:C	2.87	0.40
2:B:1004:GLY:HA2	14:N:168:LEU:HD22	2.03	0.40
2:B:1091:ARG:O	2:B:1096:SER:N	2.55	0.40
6:F:72:LYS:HD2	6:F:142:SER:CA	2.44	0.40
8:H:41:ASP:HB2	8:H:121:LEU:HB3	2.02	0.40
14:N:127:ASP:OD2	14:N:129:ALA:HB2	2.21	0.40
15:O:505:PHE:O	15:O:509:MET:HG2	2.21	0.40
16:P:185:GLN:NE2	18:R:197:PRO:CB	2.82	0.40
17:Q:10:CYS:CB	17:Q:17:SER:N	2.83	0.40
17:Q:158:MET:HA	17:Q:161:THR:HG23	2.04	0.40
18:R:173:MET:HB3	18:R:188:PHE:CZ	2.56	0.40
18:R:271:LEU:HD13	18:R:312:TYR:CB	2.51	0.40
1:A:323:ILE:O	1:A:327:VAL:HG23	2.22	0.40
1:A:454:PRO:HG2	1:A:462:LYS:HZ2	1.86	0.40
1:A:601:MET:HE1	1:A:656:GLN:HB2	2.04	0.40
2:B:371:PHE:CE2	2:B:375:LEU:HD11	2.56	0.40
2:B:498:SER:OG	2:B:723:LYS:HD3	2.22	0.40
2:B:736:ARG:NH1	2:B:738:ASP:OD1	2.54	0.40
6:F:75:PRO:CG	6:F:78:GLN:CB	2.82	0.40
15:O:107:ILE:CD1	15:O:115:LEU:HD23	2.51	0.40
16:P:377:ARG:H	16:P:377:ARG:HG3	1.64	0.40
16:P:428:GLU:CB	16:P:435:ARG:HH12	2.31	0.40
18:R:304:HIS:CE1	18:R:306:ALA:HA	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:408:LYS:HD3	1:A:408:LYS:N	2.33	0.40
1:A:581:ILE:HD12	1:A:637:PHE:CD1	2.57	0.40
1:A:1074:TYR:CE2	1:A:1159:ASP:HB3	2.54	0.40
1:A:1276:THR:HB	9:I:45:LEU:CD1	2.47	0.40
1:A:1574:ALA:HB3	9:I:122:ARG:CB	2.52	0.40
2:B:25:PHE:CD2	10:J:59:LYS:CG	3.01	0.40
2:B:31:ASP:N	2:B:176:SER:HB2	2.36	0.40
2:B:427:GLN:OE1	2:B:452:ARG:NH1	2.54	0.40
2:B:1003:ALA:C	14:N:170:HIS:HB3	2.41	0.40
3:C:326:GLU:HA	11:K:125:MET:SD	2.62	0.40
5:E:198:ILE:CD1	5:E:212:ARG:HG3	2.51	0.40
8:H:108:SER:OG	8:H:111:LEU:HD23	2.22	0.40
11:K:135:PHE:CE2	11:K:139:ILE:HD11	2.56	0.40
15:O:80:LEU:HA	15:O:81:PRO:HD3	1.86	0.40
15:O:150:TRP:O	15:O:154:VAL:HG23	2.21	0.40
16:P:198:ASP:OD1	16:P:205:TYR:O	2.39	0.40
16:P:302:VAL:HG11	16:P:362:ARG:NH1	2.30	0.40
16:P:421:ILE:HA	16:P:440:HIS:O	2.21	0.40
16:P:653:SER:H	16:P:749:LYS:HB3	1.87	0.40
17:Q:22:ILE:HD12	17:Q:26:ARG:HE	1.78	0.40
17:Q:100:ALA:HB3	17:Q:211:TYR:HE2	1.87	0.40
17:Q:118:TRP:O	17:Q:122:GLU:HB2	2.21	0.40
17:Q:129:PHE:HE1	17:Q:169:SER:N	2.19	0.40
17:Q:239:PHE:HB2	17:Q:245:SER:OG	2.21	0.40
17:Q:341:ARG:CZ	17:Q:369:TRP:CD1	3.04	0.40
1:A:597:LYS:CD	2:B:1082:HIS:CD2	3.05	0.40
1:A:670:ILE:CD1	2:B:783:MET:HE2	2.49	0.40
1:A:854:GLY:HA3	1:A:974:THR:O	2.21	0.40
1:A:1268:ASP:OD1	9:I:61:ARG:NH2	2.52	0.40
1:A:1600:ARG:NH2	1:A:1621:PHE:CE2	2.89	0.40
2:B:236:ILE:HD13	2:B:377:MET:CE	2.52	0.40
2:B:547:HIS:CB	2:B:697:LEU:O	2.69	0.40
2:B:1060:VAL:HG22	2:B:1065:ARG:NH2	2.35	0.40
2:B:1070:ARG:HH11	2:B:1070:ARG:HD2	1.75	0.40
5:E:11:ARG:HH21	5:E:141:VAL:HG21	1.87	0.40
8:H:39:THR:O	8:H:123:MET:HA	2.22	0.40
13:M:11:GLU:O	13:M:87:SER:HA	2.21	0.40
14:N:87:TYR:HA	14:N:142:THR:N	2.37	0.40
16:P:290:GLU:HB3	16:P:342:GLN:CG	2.52	0.40
16:P:470:SER:O	16:P:504:THR:HG22	2.21	0.40
17:Q:178:THR:HG22	17:Q:303:GLU:OE1	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:Q:204:ARG:NH2	17:Q:205:ILE:HD11	2.37	0.40
17:Q:474:GLU:HB3	17:Q:478:ARG:HH11	1.86	0.40
18:R:362:ALA:O	18:R:365:TRP:HB2	2.21	0.40
18:R:402:ASN:O	18:R:405:ILE:HB	2.20	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	1449/1664 (87%)	1375 (95%)	60 (4%)	14 (1%)	13 49
2	B	1164/1203 (97%)	1095 (94%)	51 (4%)	18 (2%)	8 40
3	C	303/335 (90%)	288 (95%)	12 (4%)	3 (1%)	13 49
4	D	54/137 (39%)	50 (93%)	2 (4%)	2 (4%)	2 20
5	E	210/215 (98%)	197 (94%)	11 (5%)	2 (1%)	13 49
6	F	98/155 (63%)	95 (97%)	2 (2%)	1 (1%)	13 49
7	G	187/326 (57%)	173 (92%)	12 (6%)	2 (1%)	12 47
8	H	127/146 (87%)	121 (95%)	6 (5%)	0	100 100
9	I	91/125 (73%)	80 (88%)	8 (9%)	3 (3%)	3 21
10	J	67/70 (96%)	63 (94%)	4 (6%)	0	100 100
11	K	99/142 (70%)	92 (93%)	7 (7%)	0	100 100
12	L	42/70 (60%)	36 (86%)	4 (10%)	2 (5%)	2 16
13	M	106/415 (26%)	96 (91%)	8 (8%)	2 (2%)	6 32
14	N	139/233 (60%)	123 (88%)	13 (9%)	3 (2%)	5 29
15	O	467/627 (74%)	426 (91%)	35 (8%)	6 (1%)	10 43
16	P	569/894 (64%)	474 (83%)	75 (13%)	20 (4%)	3 20

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
17	Q	398/514 (77%)	347 (87%)	41 (10%)	10 (2%)	4 26
18	R	291/507 (57%)	243 (84%)	42 (14%)	6 (2%)	5 30
All	All	5861/7778 (75%)	5374 (92%)	393 (7%)	94 (2%)	10 38

All (94) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	408	LYS
1	A	479	ALA
1	A	1651	THR
2	B	111	ASP
2	B	895	PHE
2	B	1097	ASP
3	C	224	THR
4	D	99	LEU
9	I	41	GLN
15	O	237	ILE
15	O	325	ILE
16	P	188	GLN
16	P	321	LYS
16	P	332	ASN
16	P	444	PRO
16	P	500	ILE
16	P	501	PRO
17	Q	8	PRO
17	Q	9	ILE
17	Q	15	CYS
1	A	415	ASP
1	A	448	SER
1	A	1500	GLN
1	A	1533	GLU
1	A	1606	SER
2	B	817	ARG
2	B	1049	THR
2	B	1140	LYS
4	D	98	GLY
5	E	50	MET
9	I	5	GLY
16	P	236	ILE
16	P	426	ALA
16	P	657	SER

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Mol	Chain	Res	Type
16	P	745	ALA
16	P	752	LEU
17	Q	7	GLY
17	Q	196	SER
18	R	11	ARG
18	R	267	GLY
18	R	422	GLY
1	A	69	GLU
1	A	450	LYS
2	B	78	PRO
2	B	208	VAL
2	B	209	GLN
2	B	1070	ARG
2	B	1084	THR
7	G	99	ASP
9	I	21	ASN
12	L	46	VAL
13	M	85	LYS
15	O	82	SER
15	O	469	ARG
16	P	201	GLU
16	P	241	PRO
16	P	247	ILE
16	P	666	SER
16	P	777	MET
17	Q	197	GLU
1	A	1299	ASN
2	B	834	LYS
3	C	297	HIS
7	G	100	THR
12	L	43	THR
13	M	36	THR
14	N	115	SER
15	O	130	PRO
15	O	187	MET
16	P	294	PHE
17	Q	13	ASP
1	A	451	VAL
1	A	564	PRO
2	B	80	ASN
2	B	117	VAL
2	B	1062	GLY

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Mol	Chain	Res	Type
3	C	32	ASN
5	E	146	HIS
17	Q	16	PRO
17	Q	193	PHE
18	R	249	SER
1	A	1512	PRO
2	B	1063	ARG
16	P	568	ILE
17	Q	148	PRO
18	R	362	ALA
6	F	74	ILE
14	N	70	LEU
16	P	421	ILE
18	R	295	PRO
14	N	39	PRO
2	B	833	PRO
2	B	954	PHE
16	P	203	ILE

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	1297/1465 (88%)	1215 (94%)	82 (6%)	15 36
2	B	1025/1053 (97%)	960 (94%)	65 (6%)	15 36
3	C	269/296 (91%)	253 (94%)	16 (6%)	16 37
4	D	55/116 (47%)	49 (89%)	6 (11%)	5 18
5	E	194/197 (98%)	180 (93%)	14 (7%)	12 32
6	F	90/137 (66%)	86 (96%)	4 (4%)	24 45
7	G	171/291 (59%)	159 (93%)	12 (7%)	12 32
8	H	115/128 (90%)	111 (96%)	4 (4%)	31 51
9	I	89/110 (81%)	85 (96%)	4 (4%)	23 45
10	J	64/65 (98%)	57 (89%)	7 (11%)	5 18

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
11	K	91/130 (70%)	84 (92%)	7 (8%)	10 30
12	L	39/57 (68%)	36 (92%)	3 (8%)	10 30
13	M	98/371 (26%)	85 (87%)	13 (13%)	3 13
14	N	135/220 (61%)	129 (96%)	6 (4%)	24 45
15	O	439/576 (76%)	387 (88%)	52 (12%)	4 16
16	P	539/828 (65%)	396 (74%)	143 (26%)	0 3
17	Q	383/476 (80%)	318 (83%)	65 (17%)	1 9
18	R	286/474 (60%)	228 (80%)	58 (20%)	1 6
All	All	5379/6990 (77%)	4818 (90%)	561 (10%)	8 19

All (561) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	10	GLU
1	A	40	ASN
1	A	83	VAL
1	A	117	ARG
1	A	136	LEU
1	A	174	SER
1	A	186	SER
1	A	202	THR
1	A	230	ARG
1	A	257	ASN
1	A	271	ARG
1	A	272	GLN
1	A	273	ASP
1	A	312	SER
1	A	315	ILE
1	A	346	SER
1	A	373	LEU
1	A	379	GLU
1	A	393	SER
1	A	406	LEU
1	A	407	GLN
1	A	408	LYS
1	A	410	LYS
1	A	413	LEU
1	A	414	GLU
1	A	446	ARG

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Mol	Chain	Res	Type
1	A	447	THR
1	A	451	VAL
1	A	503	VAL
1	A	555	LYS
1	A	611	GLU
1	A	627	ASP
1	A	656	GLN
1	A	661	THR
1	A	666	VAL
1	A	670	ILE
1	A	684	ASP
1	A	708	THR
1	A	709	ARG
1	A	739	VAL
1	A	747	ILE
1	A	758	GLU
1	A	783	LYS
1	A	957	VAL
1	A	966	LEU
1	A	988	SER
1	A	1026	GLN
1	A	1033	SER
1	A	1071	ASP
1	A	1085	LEU
1	A	1098	SER
1	A	1118	VAL
1	A	1123	VAL
1	A	1131	LYS
1	A	1159	ASP
1	A	1162	ASN
1	A	1204	THR
1	A	1215	VAL
1	A	1226	VAL
1	A	1273	THR
1	A	1275	THR
1	A	1276	THR
1	A	1304	GLU
1	A	1310	LYS
1	A	1314	GLN
1	A	1320	GLN
1	A	1441	LYS
1	A	1455	ARG

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Mol	Chain	Res	Type
1	A	1509	HIS
1	A	1531	ASP
1	A	1533	GLU
1	A	1536	ILE
1	A	1571	SER
1	A	1601	GLN
1	A	1604	GLU
1	A	1605	THR
1	A	1609	SER
1	A	1611	MET
1	A	1632	GLU
1	A	1633	GLN
1	A	1635	ASP
1	A	1645	LYS
2	B	17	ARG
2	B	22	GLU
2	B	53	THR
2	B	57	ASP
2	B	65	VAL
2	B	79	LEU
2	B	81	SER
2	B	87	ASN
2	B	117	VAL
2	B	150	GLU
2	B	151	ASN
2	B	187	SER
2	B	221	SER
2	B	225	ARG
2	B	228	SER
2	B	231	HIS
2	B	239	VAL
2	B	300	SER
2	B	305	ARG
2	B	306	LEU
2	B	311	ARG
2	B	315	LYS
2	B	379	ARG
2	B	459	SER
2	B	486	VAL
2	B	537	SER
2	B	583	LEU
2	B	622	ILE

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Mol	Chain	Res	Type
2	B	658	LEU
2	B	720	GLN
2	B	724	GLN
2	B	725	THR
2	B	731	VAL
2	B	753	LYS
2	B	782	ASP
2	B	811	LEU
2	B	813	LEU
2	B	819	ASP
2	B	822	THR
2	B	829	ASN
2	B	833	PRO
2	B	835	GLU
2	B	839	LYS
2	B	858	ILE
2	B	871	ILE
2	B	883	GLU
2	B	894	LYS
2	B	897	GLU
2	B	977	ILE
2	B	998	GLU
2	B	1026	ILE
2	B	1033	TYR
2	B	1037	ARG
2	B	1038	HIS
2	B	1047	ARG
2	B	1060	VAL
2	B	1075	GLU
2	B	1091	ARG
2	B	1103	VAL
2	B	1125	THR
2	B	1136	GLU
2	B	1141	LEU
2	B	1163	GLN
2	B	1165	ASN
2	B	1174	THR
3	C	38	LYS
3	C	43	ASN
3	C	50	ARG
3	C	61	THR
3	C	77	SER

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Mol	Chain	Res	Type
3	C	91	VAL
3	C	97	LEU
3	C	118	SER
3	C	142	ARG
3	C	181	ASP
3	C	224	THR
3	C	228	ARG
3	C	243	SER
3	C	245	ARG
3	C	277	ARG
3	C	279	VAL
4	D	15	THR
4	D	29	GLN
4	D	38	GLN
4	D	46	GLU
4	D	80	THR
4	D	99	LEU
5	E	31	THR
5	E	33	GLU
5	E	41	ASP
5	E	74	ASP
5	E	77	SER
5	E	90	VAL
5	E	92	THR
5	E	93	MET
5	E	107	THR
5	E	131	THR
5	E	136	ASN
5	E	142	VAL
5	E	162	ARG
5	E	177	ARG
6	F	59	GLN
6	F	87	LYS
6	F	99	LEU
6	F	109	VAL
7	G	18	LYS
7	G	24	VAL
7	G	35	SER
7	G	39	VAL
7	G	139	ILE
7	G	147	LEU
7	G	167	THR

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Mol	Chain	Res	Type
7	G	169	VAL
7	G	223	GLU
7	G	230	ARG
7	G	239	THR
7	G	243	VAL
8	H	3	ASN
8	H	39	THR
8	H	108	SER
8	H	112	ILE
9	I	2	SER
9	I	15	ASP
9	I	45	LEU
9	I	81	THR
10	J	3	VAL
10	J	9	SER
10	J	10	CYS
10	J	14	VAL
10	J	27	GLU
10	J	45	CYS
10	J	48	ARG
11	K	45	GLU
11	K	51	THR
11	K	68	GLU
11	K	99	ASN
11	K	118	GLN
11	K	123	ASP
11	K	133	SER
12	L	38	LEU
12	L	55	ILE
12	L	66	GLN
13	M	17	ASP
13	M	18	GLN
13	M	31	ARG
13	M	44	LYS
13	M	48	LYS
13	M	65	TYR
13	M	77	VAL
13	M	84	GLU
13	M	98	SER
13	M	104	SER
13	M	106	LYS
13	M	107	ASN

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Mol	Chain	Res	Type
13	M	109	ARG
14	N	51	GLN
14	N	124	THR
14	N	135	LYS
14	N	153	VAL
14	N	167	LYS
14	N	178	GLU
15	O	66	ASN
15	O	67	ASP
15	O	69	THR
15	O	78	VAL
15	O	80	LEU
15	O	87	ARG
15	O	101	SER
15	O	111	ARG
15	O	117	GLN
15	O	171	CYS
15	O	175	MET
15	O	180	LEU
15	O	181	ARG
15	O	190	ILE
15	O	192	THR
15	O	202	ASN
15	O	203	ASP
15	O	204	THR
15	O	205	ARG
15	O	212	THR
15	O	213	SER
15	O	215	LEU
15	O	225	LEU
15	O	228	GLN
15	O	232	LEU
15	O	234	ILE
15	O	239	SER
15	O	245	GLN
15	O	248	LEU
15	O	341	THR
15	O	350	GLU
15	O	354	SER
15	O	363	THR
15	O	376	TYR
15	O	381	ILE

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Mol	Chain	Res	Type
15	O	395	LEU
15	O	407	SER
15	O	410	VAL
15	O	415	GLU
15	O	437	THR
15	O	448	SER
15	O	454	VAL
15	O	489	ASN
15	O	494	THR
15	O	495	ASP
15	O	526	LEU
15	O	579	LEU
15	O	581	THR
15	O	584	GLN
15	O	597	LEU
15	O	599	LEU
15	O	602	TYR
16	P	21	GLN
16	P	26	TYR
16	P	49	THR
16	P	55	LEU
16	P	64	LEU
16	P	187	ILE
16	P	194	ARG
16	P	195	ASN
16	P	201	GLU
16	P	205	TYR
16	P	207	SER
16	P	212	SER
16	P	214	LEU
16	P	227	LEU
16	P	232	ASN
16	P	236	ILE
16	P	243	LYS
16	P	245	ILE
16	P	246	LYS
16	P	252	GLU
16	P	256	ARG
16	P	257	ARG
16	P	260	LEU
16	P	263	ILE
16	P	264	ILE

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Mol	Chain	Res	Type
16	P	266	GLU
16	P	268	SER
16	P	271	ILE
16	P	276	SER
16	P	282	CYS
16	P	290	GLU
16	P	292	LEU
16	P	300	LEU
16	P	305	PHE
16	P	314	GLN
16	P	321	LYS
16	P	329	ILE
16	P	333	PHE
16	P	343	LEU
16	P	345	ASP
16	P	347	LEU
16	P	355	GLU
16	P	356	GLU
16	P	359	SER
16	P	360	TRP
16	P	363	ILE
16	P	364	GLU
16	P	369	PHE
16	P	370	GLN
16	P	377	ARG
16	P	379	LYS
16	P	384	ASP
16	P	386	MET
16	P	388	ASN
16	P	390	GLN
16	P	397	LYS
16	P	403	ARG
16	P	407	ARG
16	P	408	ILE
16	P	410	ASP
16	P	412	ASN
16	P	415	LEU
16	P	419	ARG
16	P	421	ILE
16	P	424	VAL
16	P	430	ASN
16	P	433	VAL

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Mol	Chain	Res	Type
16	P	439	LYS
16	P	442	LEU
16	P	443	ASP
16	P	448	THR
16	P	453	VAL
16	P	455	LYS
16	P	460	ASP
16	P	463	LEU
16	P	464	LEU
16	P	465	VAL
16	P	473	HIS
16	P	474	LYS
16	P	492	LEU
16	P	494	CYS
16	P	496	THR
16	P	497	VAL
16	P	498	LEU
16	P	500	ILE
16	P	511	ILE
16	P	531	PHE
16	P	534	VAL
16	P	538	LEU
16	P	539	VAL
16	P	545	SER
16	P	555	THR
16	P	556	GLN
16	P	574	TRP
16	P	580	ASN
16	P	582	ASP
16	P	584	ARG
16	P	596	ILE
16	P	600	GLU
16	P	608	GLN
16	P	609	ASN
16	P	615	ASN
16	P	617	HIS
16	P	625	ASP
16	P	626	LEU
16	P	630	LEU
16	P	632	ILE
16	P	635	ASN
16	P	637	LEU

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Mol	Chain	Res	Type
16	P	638	LEU
16	P	646	ASP
16	P	647	GLU
16	P	654	LEU
16	P	656	HIS
16	P	659	LEU
16	P	660	LYS
16	P	662	LEU
16	P	664	GLU
16	P	665	ASN
16	P	667	ASP
16	P	671	SER
16	P	676	SER
16	P	679	LEU
16	P	693	PHE
16	P	700	LEU
16	P	703	PHE
16	P	706	GLU
16	P	711	LEU
16	P	712	ASP
16	P	726	SER
16	P	730	GLU
16	P	731	LEU
16	P	736	ILE
16	P	742	TRP
16	P	748	GLU
16	P	749	LYS
16	P	751	SER
16	P	753	PHE
16	P	757	GLN
16	P	762	ARG
16	P	768	TYR
16	P	772	ILE
16	P	777	MET
17	Q	17	SER
17	Q	21	ARG
17	Q	26	ARG
17	Q	27	ARG
17	Q	103	LEU
17	Q	110	PHE
17	Q	112	LEU
17	Q	119	LEU

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Mol	Chain	Res	Type
17	Q	138	LEU
17	Q	139	LYS
17	Q	143	THR
17	Q	144	ILE
17	Q	145	ASN
17	Q	147	GLN
17	Q	154	LEU
17	Q	159	THR
17	Q	164	ILE
17	Q	167	LEU
17	Q	169	SER
17	Q	173	SER
17	Q	176	VAL
17	Q	187	THR
17	Q	192	TYR
17	Q	204	ARG
17	Q	207	LEU
17	Q	218	SER
17	Q	220	SER
17	Q	226	LEU
17	Q	229	LYS
17	Q	232	LEU
17	Q	248	SER
17	Q	273	VAL
17	Q	286	LEU
17	Q	290	THR
17	Q	291	ASP
17	Q	292	GLU
17	Q	301	HIS
17	Q	312	LEU
17	Q	318	LEU
17	Q	328	LEU
17	Q	332	LEU
17	Q	337	SER
17	Q	348	ILE
17	Q	359	ASP
17	Q	363	SER
17	Q	366	TYR
17	Q	367	PHE
17	Q	368	GLN
17	Q	379	LYS
17	Q	384	GLN

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Mol	Chain	Res	Type
17	Q	389	GLN
17	Q	412	LYS
17	Q	419	LEU
17	Q	435	GLN
17	Q	436	LEU
17	Q	444	GLU
17	Q	445	ARG
17	Q	453	PHE
17	Q	495	LYS
17	Q	498	LEU
17	Q	502	ILE
17	Q	506	LYS
17	Q	511	HIS
17	Q	512	ARG
17	Q	513	MET
18	R	1	MET
18	R	4	VAL
18	R	8	LEU
18	R	10	ASN
18	R	11	ARG
18	R	15	GLN
18	R	28	SER
18	R	74	GLN
18	R	80	ARG
18	R	84	TRP
18	R	85	ARG
18	R	87	VAL
18	R	143	THR
18	R	149	LYS
18	R	150	GLN
18	R	155	GLN
18	R	156	LYS
18	R	160	HIS
18	R	167	LYS
18	R	168	ILE
18	R	178	LEU
18	R	181	THR
18	R	202	THR
18	R	206	ARG
18	R	209	ARG
18	R	210	THR
18	R	211	ARG

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Mol	Chain	Res	Type
18	R	212	HIS
18	R	216	LEU
18	R	218	ASP
18	R	231	LEU
18	R	235	ILE
18	R	238	THR
18	R	242	ILE
18	R	247	ILE
18	R	248	LYS
18	R	250	LEU
18	R	255	VAL
18	R	266	SER
18	R	269	ASP
18	R	272	GLN
18	R	298	GLN
18	R	299	THR
18	R	302	ARG
18	R	308	PHE
18	R	312	TYR
18	R	313	LEU
18	R	319	ASN
18	R	322	LYS
18	R	323	SER
18	R	345	LEU
18	R	347	ASP
18	R	364	VAL
18	R	367	ILE
18	R	373	LEU
18	R	374	LEU
18	R	410	TYR
18	R	420	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (38) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	382	GLN
1	A	407	GLN
1	A	425	ASN
1	A	470	HIS
1	A	535	GLN
1	A	1162	ASN
1	A	1314	GLN

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Mol	Chain	Res	Type
1	A	1320	GLN
2	B	146	ASN
2	B	182	GLN
2	B	462	GLN
2	B	554	GLN
2	B	702	ASN
2	B	1163	GLN
7	G	126	GLN
7	G	154	ASN
12	L	53	HIS
15	O	66	ASN
15	O	70	GLN
15	O	105	ASN
15	O	210	ASN
15	O	245	GLN
15	O	342	HIS
15	O	362	ASN
15	O	371	HIS
15	O	390	GLN
15	O	488	HIS
15	O	497	ASN
15	O	521	ASN
15	O	547	ASN
15	O	549	ASN
16	P	228	ASN
16	P	348	HIS
16	P	461	HIS
16	P	473	HIS
17	Q	406	GLN
18	R	184	ASN
18	R	212	HIS

5.3.3 RNA (i)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains (i)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 14 ligands modelled in this entry, 9 are monoatomic - leaving 5 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
20	SO4	R	601	18	4,4,4	0.17	0	6,6,6	0.11	0
20	SO4	P	902	-	4,4,4	0.14	0	6,6,6	0.23	0
20	SO4	Q	1002	-	4,4,4	0.14	0	6,6,6	0.26	0
20	SO4	P	903	-	4,4,4	0.14	0	6,6,6	0.10	0
20	SO4	P	901	-	4,4,4	0.11	0	6,6,6	0.24	0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
20	R	601	SO4	4	0
20	P	902	SO4	1	0
20	Q	1002	SO4	1	0
20	P	903	SO4	1	0

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	2
7	G	1
9	I	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	G	24:VAL	C	25:THR	N	4.53
1	I	45:LEU	C	46:LYS	N	3.17
1	A	438:ILE	C	439:ASP	N	2.97
1	A	991:LYS	C	992:PRO	N	2.86

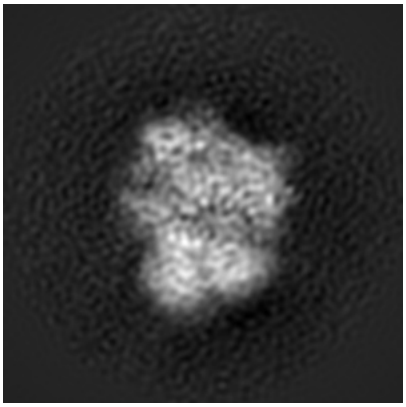
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-3590. These allow visual inspection of the internal detail of the map and identification of artifacts.

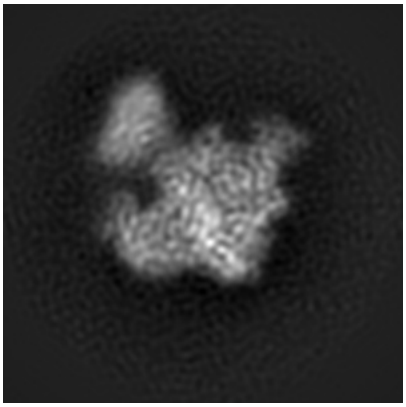
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

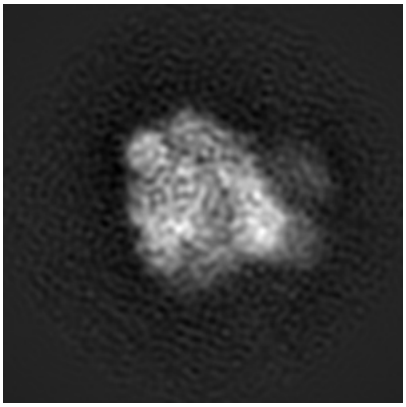
6.1.1 Primary map



X



Y

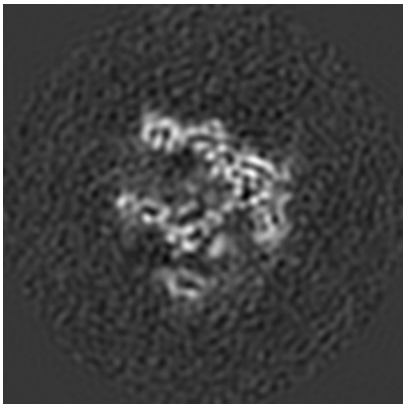


Z

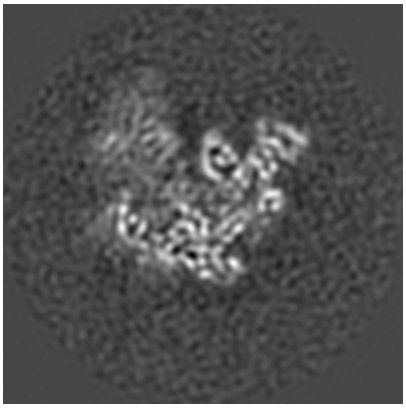
The images above show the map projected in three orthogonal directions.

6.2 Central slices

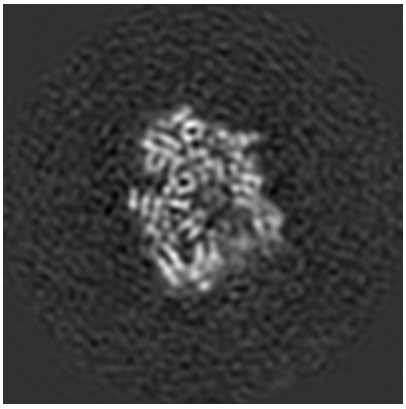
6.2.1 Primary map



X Index: 120



Y Index: 120

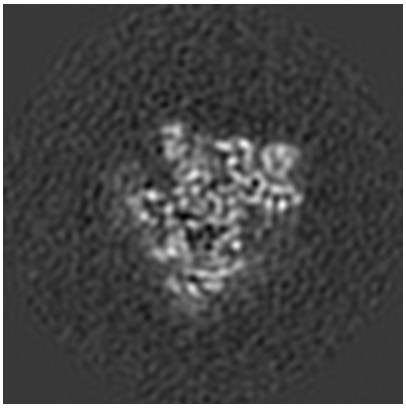


Z Index: 120

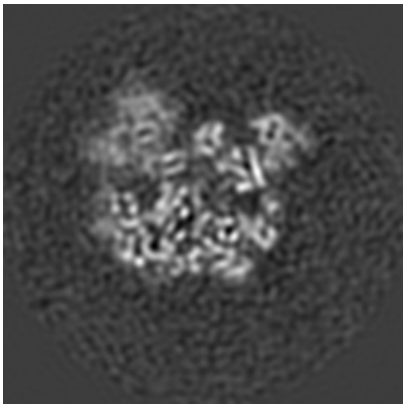
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

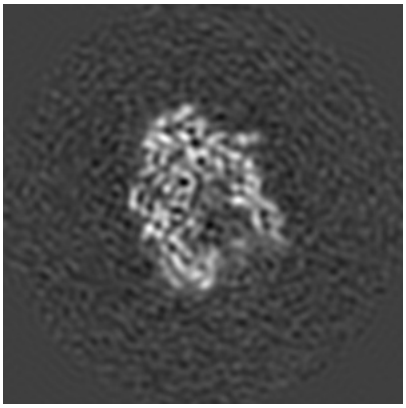
6.3.1 Primary map



X Index: 111



Y Index: 109

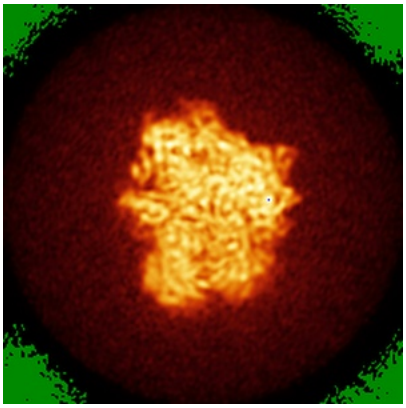


Z Index: 122

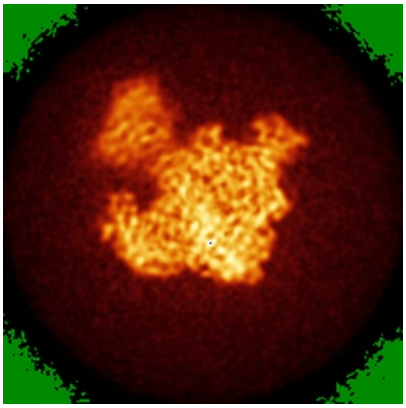
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

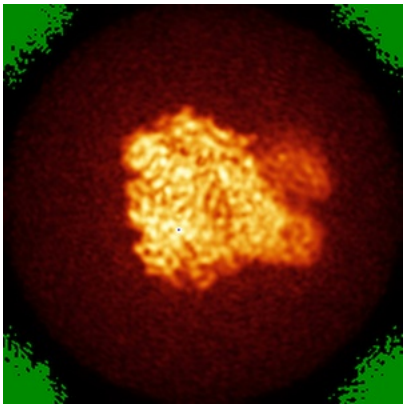
6.4.1 Primary map



X



Y

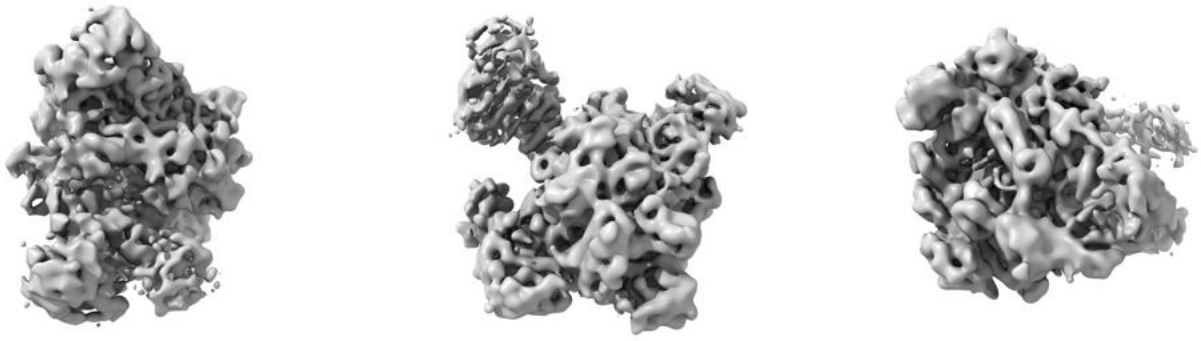


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views (i)

6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.0205. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

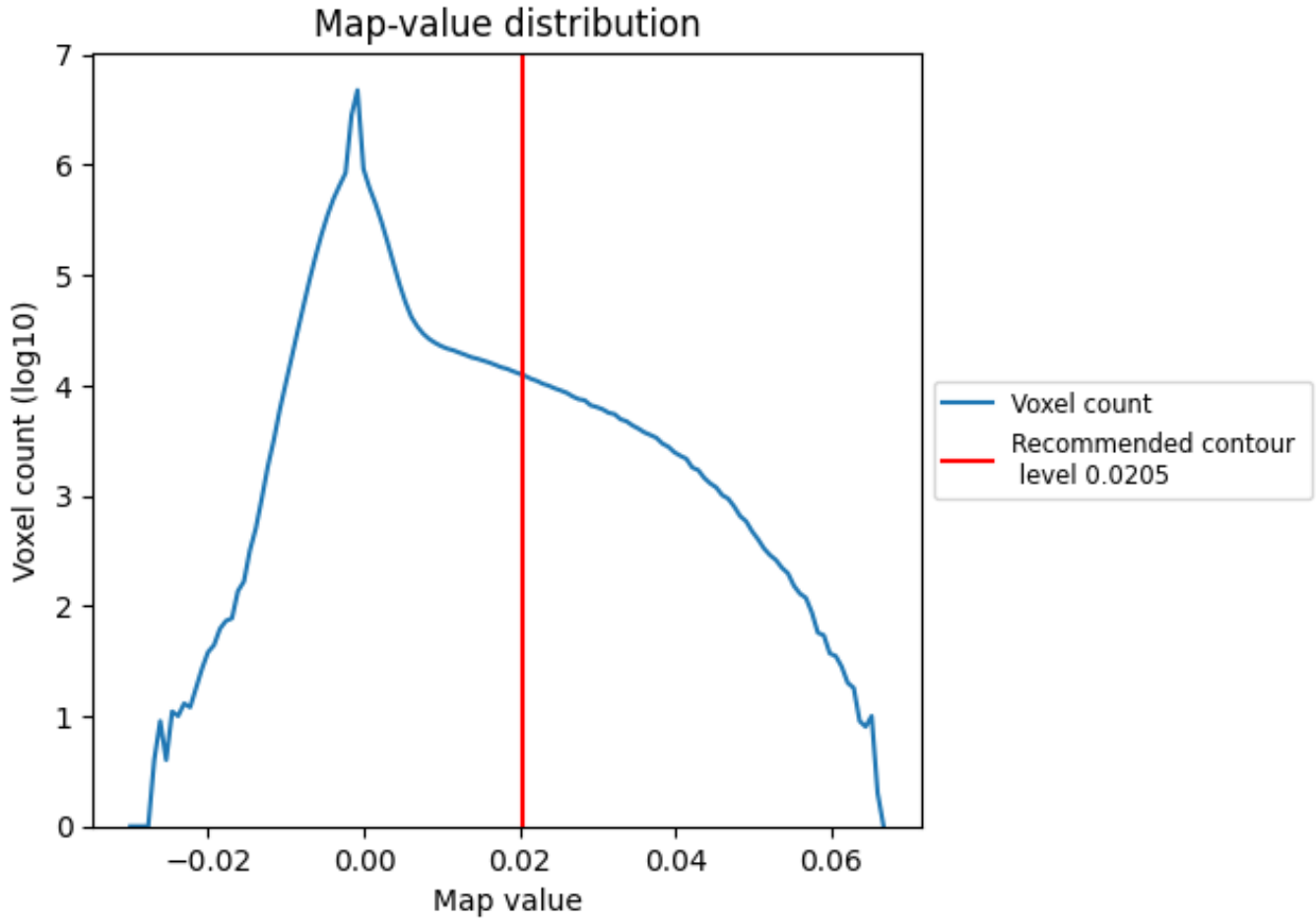
6.6 Mask visualisation (i)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis

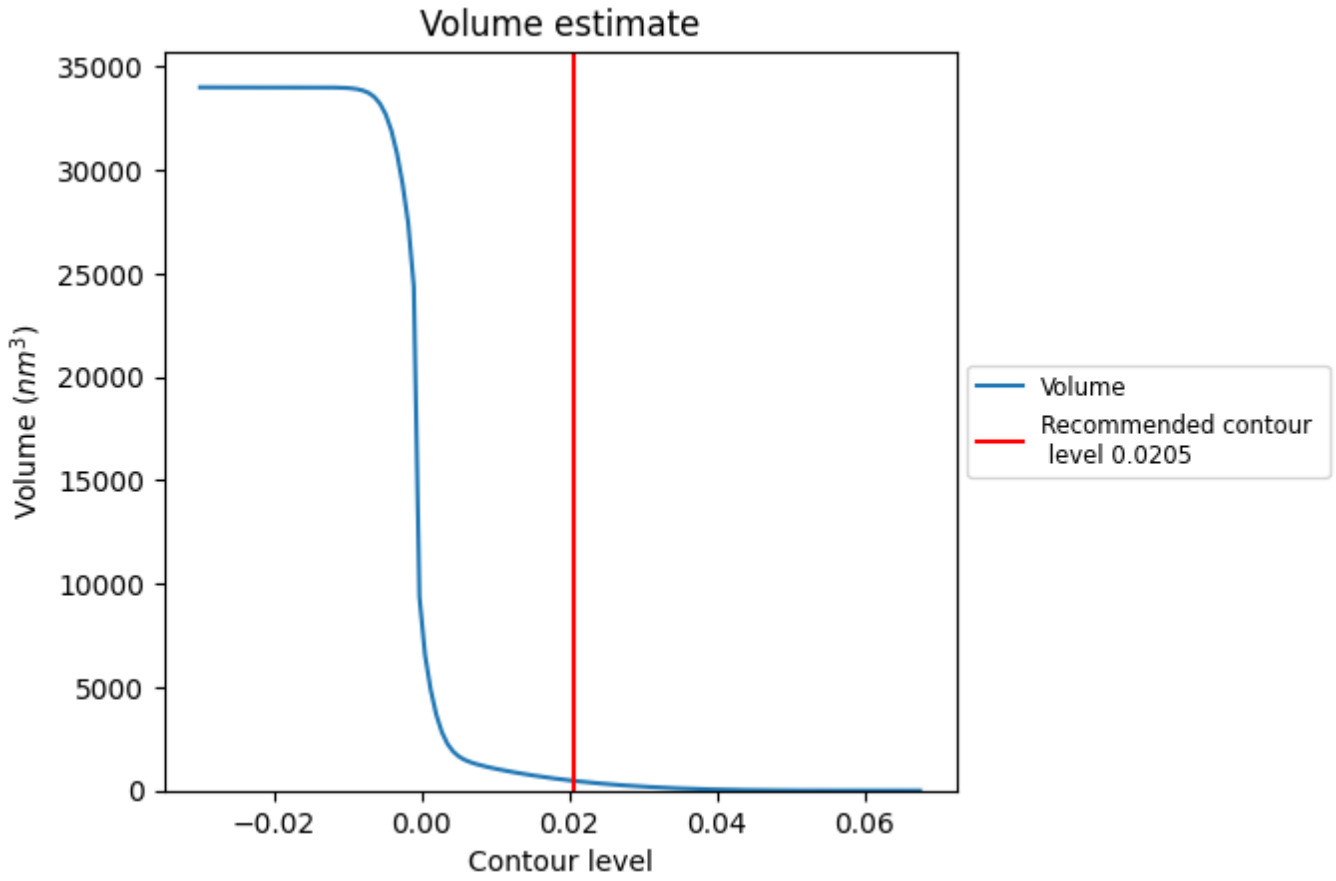
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

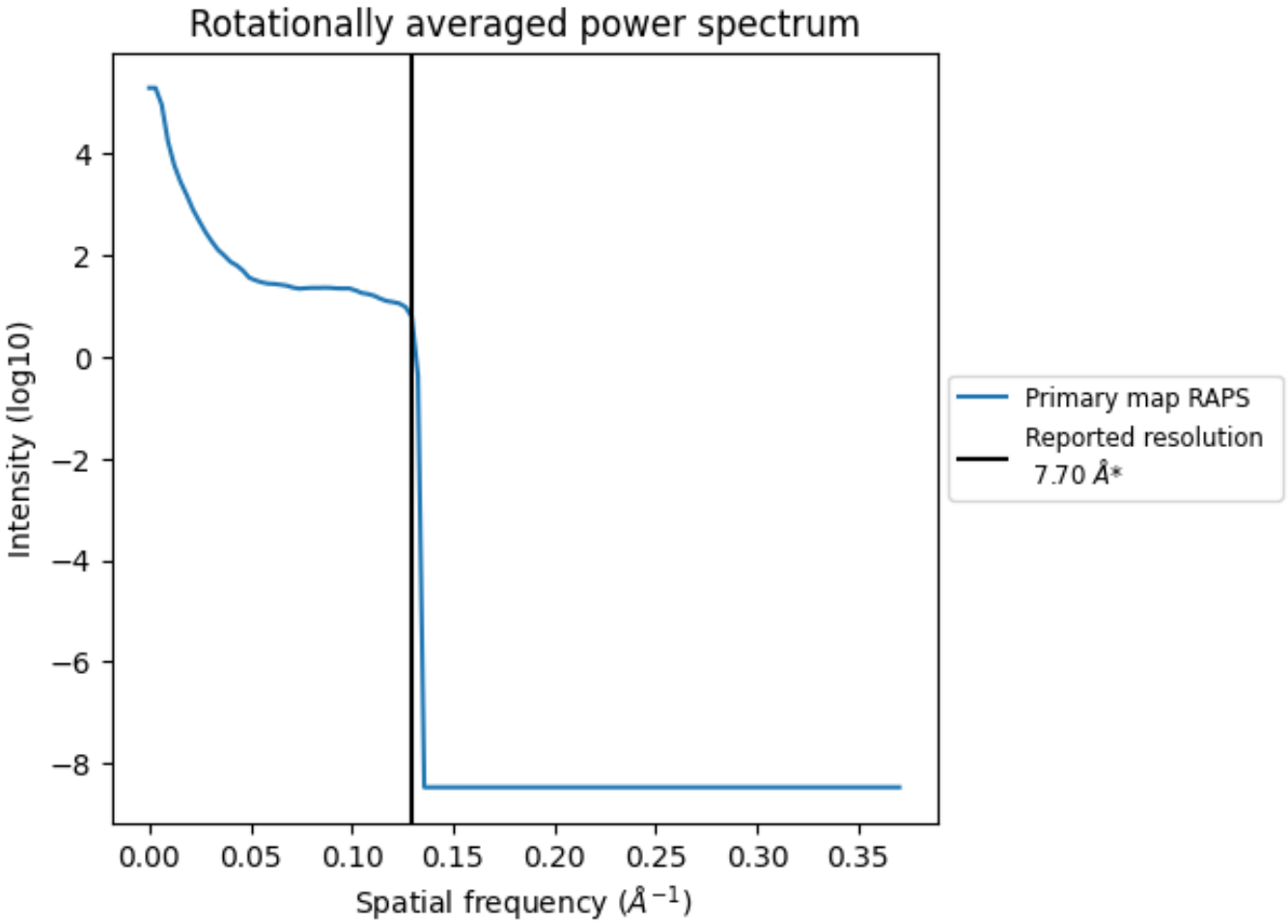
7.2 Volume estimate



The volume at the recommended contour level is 475 nm^3; this corresponds to an approximate mass of 429 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum (i)



*Reported resolution corresponds to spatial frequency of 0.130 Å^{-1}

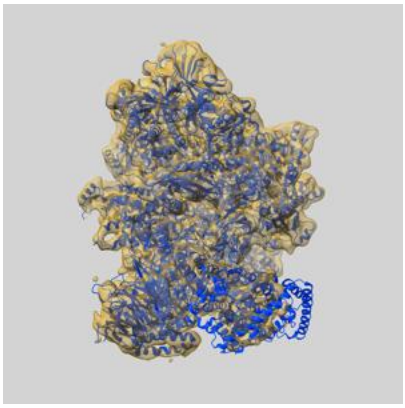
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

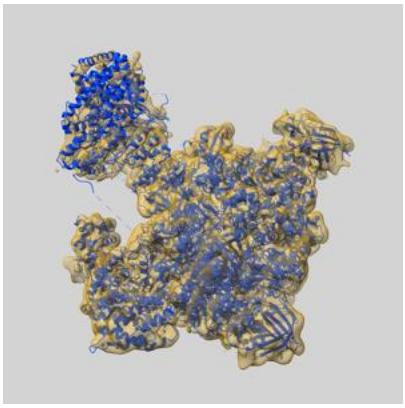
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-3590 and PDB model 5N5Y. Per-residue inclusion information can be found in section 3 on page 8.

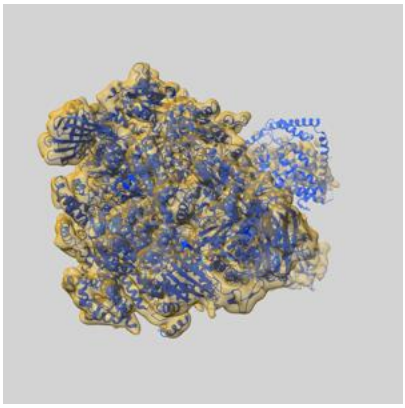
9.1 Map-model overlay



X



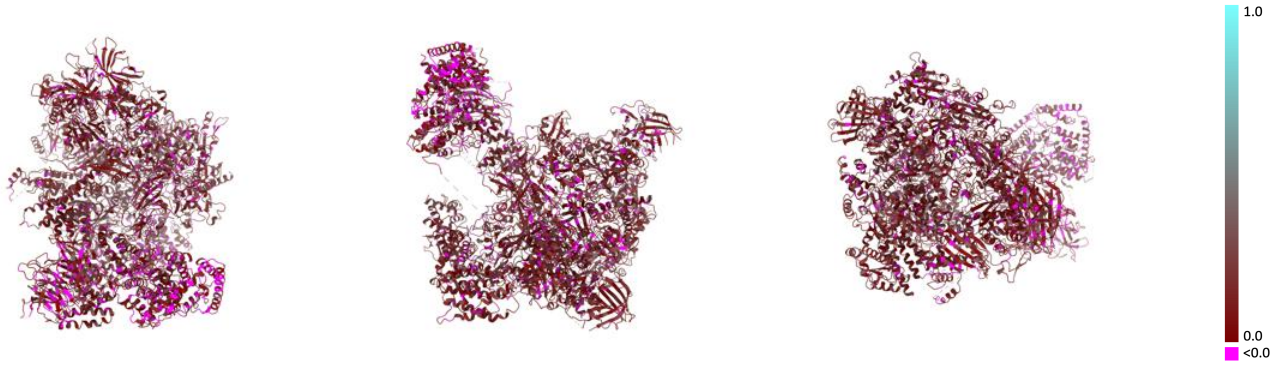
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.0205 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

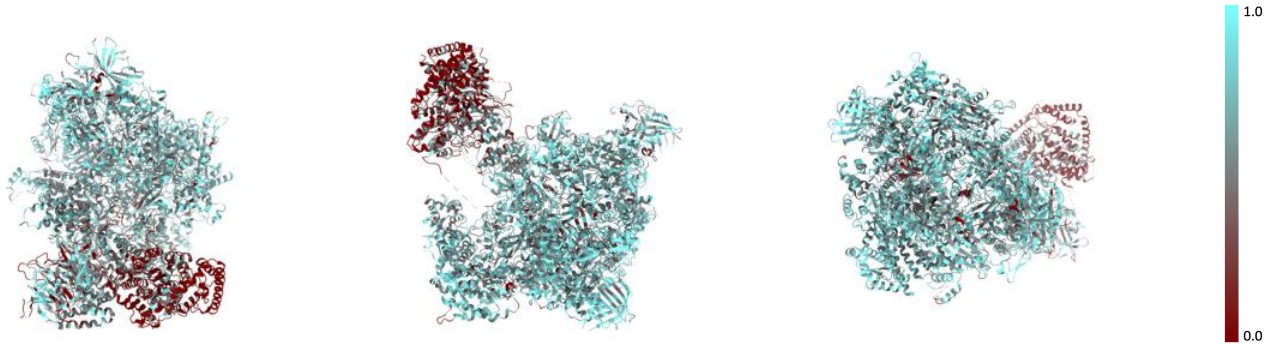
9.2 Q-score mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

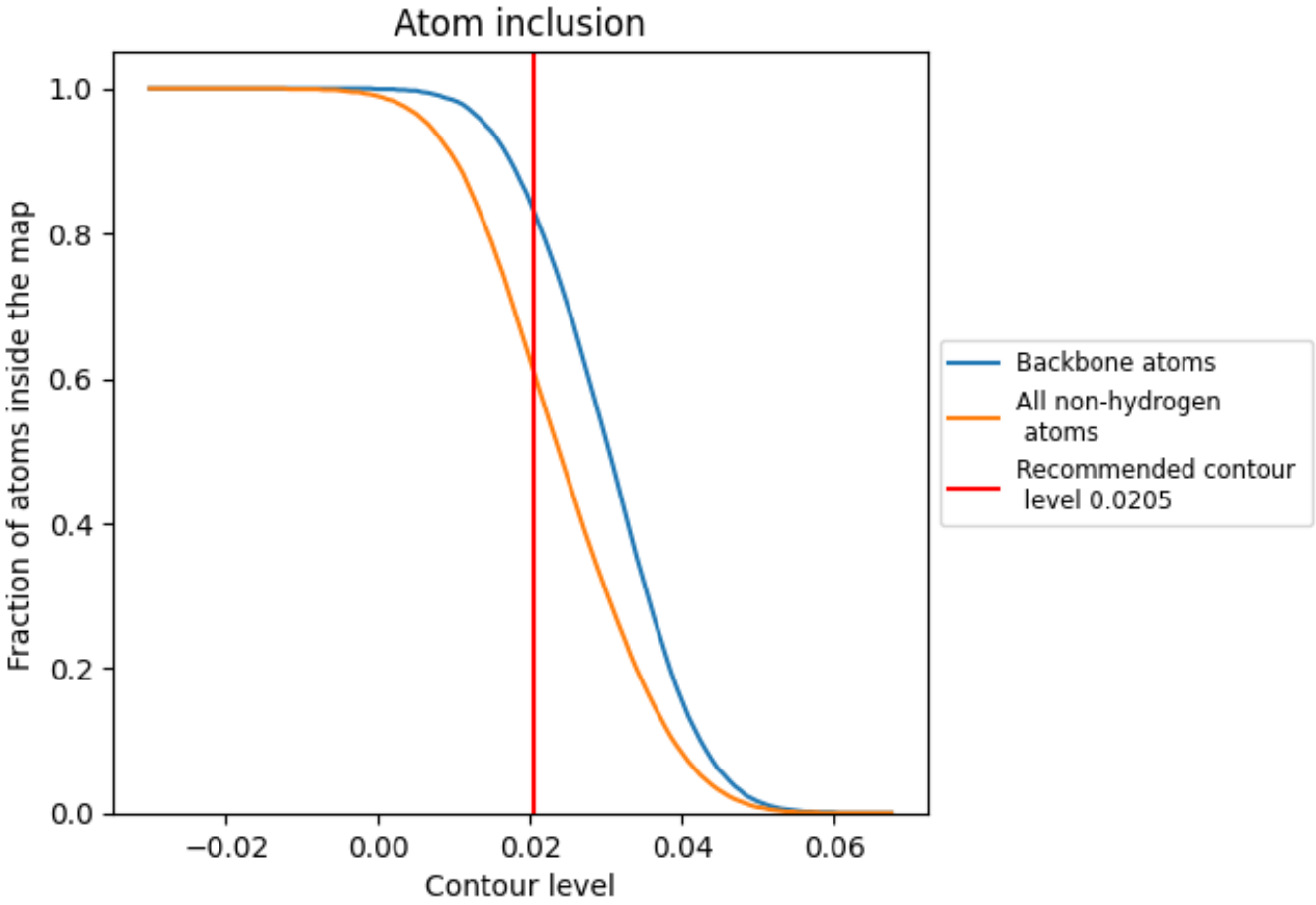
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.0205).

9.4 Atom inclusion (i)



At the recommended contour level, 83% of all backbone atoms, 61% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.0205) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6090	0.1360
A	0.6710	0.1450
B	0.6630	0.1390
C	0.7390	0.1510
D	0.7010	0.1650
E	0.7490	0.1640
F	0.6800	0.1590
G	0.7360	0.1430
H	0.7800	0.1650
I	0.4990	0.1470
J	0.7050	0.1390
K	0.7080	0.1590
L	0.6560	0.1360
M	0.6540	0.1420
N	0.6120	0.1470
O	0.6660	0.1450
P	0.3550	0.0870
Q	0.2790	0.0930
R	0.5080	0.1370